

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 6, 2006, 16:50:52 ; Search time 114 Seconds
(without alignments)
34.688 Million cell updates/sec

Title: US-10-791-217A-1

Perfect score: 37

Sequence: 1 VLXDDLLEA 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 770462

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21:*

1: geneeqp1980s:*
2: geneeqp1990s:*
3: geneeqp2000s:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003as:*
7: geneeqp2003bs:*
8: geneeqp2004s:*
9: geneeqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	36	97.3	9	2	AAW99195
2	36	97.3	9	2	AAW99196
3	36	97.3	9	2	AAW99197
4	36	97.3	9	2	AAW97572
5	36	97.3	9	2	AAW97575
6	36	97.3	9	2	AAW97374
7	36	97.3	9	8	ADH40333
8	36	97.3	9	8	ADH40334
9	36	97.3	13	2	AAW99199
10	36	97.3	13	2	AAW99198
11	36	97.3	13	2	AAW97415
12	36	97.3	13	2	AAW97414
13	28	75.7	10	6	ABP71119
14	26	70.3	10	8	ADT73023
15	26	70.3	10	2	AAW73501
16	25	67.6	10	4	AAW94234
17	25	67.6	10	4	ADQ26722
18	25	67.6	11	7	ADD23269
19	25	67.6	12	2	AAW64577
20	25	67.6	13	5	ADG66269
21	25	67.6	13	5	ADG66272
22	25	67.6	13	5	ADG66271
23	25	67.6	13	5	ADG66270
24	25	67.6	15	5	ABB07889

25	24	64.9	9	8	ABY01546
26	24	64.9	9	9	ADZ50925
27	24	64.9	10	6	ABR04849
28	24	64.9	10	8	ABY01491
29	24	64.9	10	9	ADY49658
30	24	64.9	10	9	ADY49658
31	24	64.9	13	6	AAE34759
32	24	64.9	13	7	ADD23767
33	24	64.9	14	7	ADD23419
34	24	64.9	15	6	ABR30509
35	24	64.9	15	6	ABR30940
36	24	64.9	15	6	ABR31271
37	24	64.9	15	6	ABR30473
38	24	64.9	15	6	ABR30612
39	24	64.9	15	6	ABR31028
40	24	64.9	15	6	ABR30613
41	24	64.9	15	6	ABR31170
42	24	64.9	15	6	ABR30941
43	24	64.9	15	6	ABR31063
44	24	64.9	15	6	ABR31169
45	24	64.9	15	6	ABR31559

ALIGNMENTS

RESULT 1	
ID	AAW99195
standard; peptide; 9 AA.	
AAW99195;	
20-MAY-1999 (first entry)	
Minor histocompatibility antigen HA-1 T-cell epitope #1.	
Minor histocompatibility antigen; HA-1; T-cell epitope; immunological; graft versus host disease; bone marrow transplant; leukaemia; vaccine; diagnosis; aplastic anaemia; immune deficiency disease.	
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FT	Key
FT	Misc-difference 3 /label= His, Arg
XX	
XX	WO9905174-A1.
XX	04-FEB-1999.
XX	23-JUL-1998; 98WO-NL000425.
XX	23-JUL-1997; 97EP-00202303.
XX	(UYLE-) RIJKSUNIV LEIDEN.
XX	Goulimy EAMV, Hunt DF, Engelhard VH;
XX	WPI, 1999-153312/13.
XX	A new minor histocompatibility antigen, HA-1 - useful to treat immune diseases and prevent rejection and host versus graft disease in bone marrow and organ transplantation.
XX	Claim 1; Page 32; 47pp; English.
XX	The present sequence represents a new peptide (PI) constituting a T-cell epitope obtainable from the minor histocompatibility antigen HA-1. The peptide is immunogenic and can be used as part of a vaccine. PI is used as a medicine, to induce tolerance for transplants, prevent rejection and/or graft versus host disease, or to treat (auto) immune diseases. In particular it can be used with bone marrow transplantation, in the

CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases
XX
SQ Sequence 9 AA;
Query Match 97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLXDDLLEA 9
|||
1 VLXDDLLEA 9
Db 1 VLXDDLLEA 9
RESULT 2
AAW9196
ID AAW9196 standard; peptide; 9 AA.
AC AAW9196;
XX
XX 20-MAY-1999 (first entry)
DT
XX Minor histocompatibility antigen HA-1 T-cell epitope #2.
DE
XX Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KM diagnosis; aplastic anaemia; immune deficiency disease.
XX
XX Homo sapiens.
OS
XX W09905174-A1.
PN
XX 04-FEB-1999.
PD
XX 23-JUL-1998; 98WO-NL000425.
PF
XX 23-JUL-1997; 97EP-00202303.
PR
XX (UYLE-) RIJKSUNIV LEIDEN.
PA
XX Goulmy EAJM, Hunt DF, Engelhard VH;
PI
XX WPI; 1999-153312/13.
DR
XX A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
PS
XX Claim 3; Page 32; 47pp; English.
XX
CC The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases
CC
SQ Sequence 9 AA;
Query Match 97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VLXDDLLEA 9
|||
1 VLXDDLLEA 9
Db 1 VLXDDLLEA 9
RESULT 3
AAW9197
ID AAW9197 standard; peptide; 9 AA.

XX AAW9197;
AC
XX 20-MAY-1999 (first entry)
DT
XX Minor histocompatibility antigen HA-1 T-cell epitope #3.
DE
XX Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KM diagnosis; aplastic anaemia; immune deficiency disease.
XX
XX Homo sapiens.
OS
XX W09905174-A1.
PN
XX 04-FEB-1999.
PD
XX 23-JUL-1998; 98WO-NL000425.
PF
XX 23-JUL-1997; 97EP-00202303.
PR
XX (UYLE-) RIJKSUNIV LEIDEN.
PA
XX Goulmy EAJM, Hunt DF, Engelhard VH;
PI
XX WPI; 1999-153312/13.
DR
XX A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
PS
XX Disclosure; Page 15; 47pp; English.
XX
CC The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases
CC
SQ Sequence 9 AA;
Query Match 97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VLXDDLLEA 9
|||
1 VLXDDLLEA 9
Db 1 VLXDDLLEA 9
RESULT 4
AAW97572
ID AAW97572 standard; peptide; 9 AA.
AC AAW97572;
XX
XX 20-MAY-1999 (first entry)
DT
XX T-cell epitope from the minor histocompatibility antigen HA-1.
DE
XX T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
KW transplant rejection; Graft-versus-Host Disease; autoimmune disease;
KM neoplastic haematopoietic cell.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 3
FT /note= "His or Arg"
XX

PN W09905173-A1.
 XX 04-FEB-1999.
 XX
 XX
 PF 23-JUL-1998; 98WO-NL000424.
 XX
 XX 23-JUL-1997; 97EP-00202303.
 XX
 XX (UYLE-) RIKKSUNIV LEIDEN.
 XX
 XX
 PI Goulmy EAJM, Hunt DF, Engelhard VH;
 XX WPI; 1999-142855/12.
 DR
 XX
 PT Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
 PT for inducing tolerance to transplants and prevent rejection or graft-
 PT versus-host disease.
 XX
 XX
 XX Claim 1; Page 39; 57pp; English.
 XX
 XX
 CC The present sequence represents an immunogenic peptide constituting a T-
 CC cell epitope, obtainable from the minor histocompatibility antigen HA-1.
 CC The peptide can be used in vaccines or pharmaceutical formulations as
 CC medicines to induce tolerance for transplants so as to prevent rejection
 CC and/or Graft-versus-host disease, or to treat autoimmune diseases.
 CC Neoplastic haematopoietic cells presenting the peptides, in an HLA class
 CC I context, can be eliminated after specific recognition of the peptides.
 CC The peptides can also be used to raise antibodies, T-cell receptor, B-
 CC and T-cells
 CC
 SQ Sequence 9 AA;

Query Match 97.3%; Score 36; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
 |||||
 1 VLXDDLLEA 9

Db

RESULT 5
 AAM97375
 ID AAM97375 standard; protein; 9 AA.
 XX
 AC AAM97375;
 XX
 DT 13-MAY-1999 (first entry)
 XX
 DE HA-1 H-allele sequence.
 XX
 XX Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
 KW R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
 KW severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
 XX
 OS Homo sapiens.
 XX
 XX W09905313-A2.
 XX
 PD 04-FEB-1999.
 XX
 XX
 PF 23-JUL-1998; 98WO-EP004928.
 XX
 XX 23-JUL-1997; 97EP-00202303.
 PR 02-JUN-1998; 98EP-00870125.
 XX
 XX (UYLE-) RIKKSUNIV LEIDEN.
 XX
 XX Goulmy E;
 PI
 DR WPI; 1999-142960/12.
 XX
 PT Typing minor histocompatibility antigen HA-1 - by amplifying and

PT Identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
 PT of genetic aberrances.
 XX
 XX
 XX Claim 18; Fig 5; 59pp; English.
 PS
 XX
 CC The present sequence represents part of the minor histocompatibility
 CC antigen HA-1 H-allele. The specification describes methods for typing
 CC alleles (preferably the H and R alleles) of the minor histocompatibility
 CC antigen HA-1 in a sample, which comprise detecting polymorphic
 CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
 CC methods can be used for HA-1 typing for bone marrow transplants, severe
 CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
 CC detection of genetic aberrances. The probes and primers of the invention
 CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
 CC anti-idiotypic B cells and/or T cells and antibodies
 CC
 SQ Sequence 9 AA;

Query Match 97.3%; Score 36; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
 |||||
 1 VLXDDLLEA 9

Db

RESULT 6
 AAM97374
 ID AAM97374 standard; protein; 9 AA.
 XX
 AC AAM97374;
 XX
 DT 13-MAY-1999 (first entry)
 XX
 DE HA-1 R-allele sequence.
 XX
 XX Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
 KW R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
 KW severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
 XX
 OS Homo sapiens.
 XX
 XX W09905313-A2.
 XX
 PD 04-FEB-1999.
 XX
 XX
 PF 23-JUL-1998; 98WO-EP004928.
 XX
 XX 23-JUL-1997; 97EP-00202303.
 PR 02-JUN-1998; 98EP-00870125.
 XX
 XX (UYLE-) RIKKSUNIV LEIDEN.
 XX
 XX Goulmy E;
 PI
 DR WPI; 1999-142960/12.
 XX
 PT Typing minor histocompatibility antigen HA-1 - by amplifying and
 PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
 PT of genetic aberrances.
 XX
 XX Claim 13; Fig 5; 59pp; English.
 PS
 XX
 CC The present sequence represents part of the minor histocompatibility
 CC antigen HA-1 R-allele. The specification describes methods for typing
 CC alleles (preferably the H and R alleles) of the minor histocompatibility
 CC antigen HA-1 in a sample, which comprise detecting polymorphic
 CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
 CC methods can be used for HA-1 typing for bone marrow transplants, severe
 CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
 CC detection of genetic aberrances. The probes and primers of the invention
 CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used

CC anti-idiotypic B cells and/or T cells and antibodies
XX
SQ Sequence 9 AA;
Query Match 97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 VLXDDLEA 9
DB 1 VLRDDLEA 9
RESULT 7
ID ADH40333 standard; peptide; 9 AA.
AC ADH40333;
XX 11-MAR-2004 (first entry)
DT Human minor histocompatibility antigen HA-1 T cell epitope.
DE human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
XX minor histocompatibility antigen; mHAg; T cell epitope.
KM Homo sapiens.
XX WO2003106692-A2.
XX 24-DEC-2003.
PD 13-JUN-2003; 2003WO-EP006251.
PP 13-JUN-2002; 2002EP-00013423.
XX 13-JUN-2002; 2002EP-00013423.
PR (MERK) MERCK PATENT GMBH.
XX (MERK) MERCK PATENT GMBH.
PA Strittmatter W, Moll H;
XX Strittmatter W, Moll H;
PI WPI; 2004-082200/08.
DR Providing allelic variant epitope of protein based on single nucleotide
XX polymorphism by defining target protein, screening database of protein,
PT identifying, selecting allelic variant protein, creating variant
PT epitopes.
XX
XX Disclosure; Page 82; 119pp; English.
PS The invention relates to a novel method for providing epitopes of allelic
XX variants of antigenic proteins from specific species based on single
XX nucleotide polymorphism (SNP), by defining target protein/peptide or its
XX subset, screening database of DNA encoding target protein, identifying,
XX selecting allelic peptide/protein variants, expression product or its
XX fragment encoded by DNA sequence having SNP, creating variant epitopes,
XX selecting epitopes binding to MHC protein, A protein of the invention has
XX cytostatic activity, and may have a use in a vaccine. The method is
XX useful for generating a SNP profile of one or more individuals from a
XX given species by applying the method for several protein from the
XX individuals, where the SNP profile was related to disease, preferably
XX cancer. This is useful for diagnosing a disease in an individual by
XX generating the SNP-related polymorphic profile. A method of the invention
XX is useful for transplanting haematopoietic stem cells from a donor to a
XX recipient and treating cancer, preferably leukaemia, and for determining
XX the progression, regression or onset of a treated disease. The present
XX sequence is used in the exemplification of the invention.
SQ Sequence 9 AA;
Query Match 97.3%; Score 36; DB 8; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLXDDLEA 9
DB 1 VLRDDLEA 9
RESULT 8
ID ADH40334 standard; peptide; 9 AA.
AC ADH40334;
XX 11-MAR-2004 (first entry)
DT Human minor histocompatibility antigen HA-1 T cell epitope.
DE human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
XX minor histocompatibility antigen; mHAg; T cell epitope.
KM Homo sapiens.
XX WO2003106692-A2.
XX 24-DEC-2003.
PD 13-JUN-2003; 2003WO-EP006251.
PP 13-JUN-2002; 2002EP-00013423.
XX 13-JUN-2002; 2002EP-00013423.
PR (MERK) MERCK PATENT GMBH.
XX (MERK) MERCK PATENT GMBH.
PA Strittmatter W, Moll H;
XX Strittmatter W, Moll H;
PI WPI; 2004-082200/08.
DR Providing allelic variant epitope of protein based on single nucleotide
XX polymorphism by defining target protein, screening database of protein,
PT identifying, selecting allelic variant protein, creating variant
PT epitopes.
XX
XX Disclosure; Page 82; 119pp; English.
PS The invention relates to a novel method for providing epitopes of allelic
XX variants of antigenic proteins from specific species based on single
XX nucleotide polymorphism (SNP), by defining target protein/peptide or its
XX subset, screening database of DNA encoding target protein, identifying,
XX selecting allelic peptide/protein variants, expression product or its
XX fragment encoded by DNA sequence having SNP, creating variant epitopes,
XX selecting epitopes binding to MHC protein, A protein of the invention has
XX cytostatic activity, and may have a use in a vaccine. The method is
XX useful for generating a SNP profile of one or more individuals from a
XX given species by applying the method for several protein from the
XX individuals, where the SNP profile was related to disease, preferably
XX cancer. This is useful for diagnosing a disease in an individual by
XX generating the SNP-related polymorphic profile. A method of the invention
XX is useful for transplanting haematopoietic stem cells from a donor to a
XX recipient and treating cancer, preferably leukaemia, and for determining
XX the progression, regression or onset of a treated disease. The present
XX sequence is used in the exemplification of the invention.
SQ Sequence 9 AA;
Query Match 97.3%; Score 36; DB 8; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 VLXDDLEA 9
DB 1 VLRDDLEA 9
RESULT 9
ID AAW9199 standard; peptide; 13 AA.


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XX AC AAW99199;
XX XX
XX DT 20-MAY-1999 (first entry)
XX XX
XX DE VR cell KIAA0223 protein sequence.
XX XX
XX KW Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
XX KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
XX KW diagnosis; aplastic anaemia; immune deficiency disease.
XX OS Synthetic.
XX PN WO9905174-A1.
XX PD 04-FEB-1999.
XX PF 23-JUL-1998; 98WO-NL000425.
XX PR 23-JUL-1997; 97EP-00202303.
XX PA (UYLE-) RIKKSUNIV LEIDEN.
XX PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX DR WPI; 1999-153312/13.
XX DR N-PSDB; AAX19409.
XX PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
XX PT diseases and prevent rejection and host versus graft disease in bone
XX PT marrow and organ transplantation.
XX PS Disclosure; Page 31; 47pp; English.
XX CC The present invention describes a new peptide (P1) constituting a T-cell
XX CC epitope obtainable from the minor histocompatibility antigen HA-1. The
XX CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
XX CC as a medicine, to induce tolerance for transplants, prevent rejection
XX CC and/or graft versus host disease, or to treat (auto) immune diseases. In
XX CC particular it can be used with bone marrow transplantation, in the
XX CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
XX CC diseases. The present sequence represents a KIAA0223 sequence given in
XX CC the present invention
XX SQ Sequence 13 AA;

Query Match 97.3%; Score 36; DB 2; Length 13;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLKDDLLEA 9
   |||||
Db 3 VLHDDLLEA 11

RESULT 10
AAW99198
ID AAW99198 standard; peptide; 13 AA.
XX AC AAW99198;
XX DT 20-MAY-1999 (first entry)
XX DE DH cell KIAA0223 protein sequence.
XX KW Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
XX KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
XX KW diagnosis; aplastic anaemia; immune deficiency disease.
XX OS Synthetic.
XX PN WO9905174-A1.
XX PT

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PD 04-FEB-1999.
XX XX
XX PF 23-JUL-1998; 98WO-NL000425.
XX PR 23-JUL-1997; 97EP-00202303.
XX PA (UYLE-) RIKKSUNIV LEIDEN.
XX PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX DR WPI; 1999-153312/13.
XX DR N-PSDB; AAX19408.
XX PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
XX PT diseases and prevent rejection and host versus graft disease in bone
XX PT marrow and organ transplantation.
XX PS Disclosure; Page 31; 47pp; English.
XX CC The present invention describes a new peptide (P1) constituting a T-cell
XX CC epitope obtainable from the minor histocompatibility antigen HA-1. The
XX CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
XX CC as a medicine, to induce tolerance for transplants, prevent rejection
XX CC and/or graft versus host disease, or to treat (auto) immune diseases. In
XX CC particular it can be used with bone marrow transplantation, in the
XX CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
XX CC diseases. The present sequence represents a KIAA0223 sequence given in
XX CC the present invention
XX SQ Sequence 13 AA;

Query Match 97.3%; Score 36; DB 2; Length 13;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLKDDLLEA 9
   |||||
Db 3 VLHDDLLEA 11

RESULT 11
AAW97415
ID AAW97415 standard; protein; 13 AA.
XX AC AAW97415;
XX DT 20-MAY-1999 (first entry)
XX DE KIAA0223 polymorphism in HA-1 positive homozygous individuals.
XX KW T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
XX KW transplant rejection; Graft-versus-Host Disease; autoimmune disease;
XX KW neoplastic haematopoietic cell; KIAA0223 polymorphism.
XX OS Homo sapiens.
XX PN WO9905173-A1.
XX PD 04-FEB-1999.
XX PF 23-JUL-1998; 98WO-NL000424.
XX PR 23-JUL-1997; 97EP-00202303.
XX PA (UYLE-) RIKKSUNIV LEIDEN.
XX PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX DR WPI; 1999-142855/12.
XX DR N-PSDB; AAX16081.
XX PT Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
XX PT for inducing tolerance to transplants and prevent rejection or graft-

```

PT versus-host disease.
 XX
 XX Disclousure; Page 38; 57pp; English.
 PS
 CC The present sequence represents the KIAA0223 polymorphism in HA-1
 CC positive homozygous individuals. The specification describes an
 CC immunogenic peptide constituting a T-cell epitope, obtainable from the
 CC minor histocompatibility antigen HA-1. The peptide can be used in
 CC vaccines or pharmaceutical formulations as medicines to induce tolerance
 CC for transplants so as to prevent rejection and/or Graft-versus-Host
 CC disease, or to treat autoimmune diseases. Neoplastic haematopoietic cells
 CC presenting the peptides, in an HLA class I context, can be eliminated
 CC after specific recognition of the peptides. The peptides can also be used
 CC to raise antibodies, T-cell receptor, B- and T-cells
 CC
 XX
 SQ Sequence 13 AA;
 Query Match 97.3%; Score 36; DB 2; Length 13;
 Best Local Similarity 88.9%; Pred. No. 1.8; 1; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 VLXDDLLEA 9
 |||||
 Db 3 VLHDDLLEA 11
 RESULT 12
 AAM97414
 ID AAW97414 standard; protein; 13 AA.
 XX
 AC AAM97414;
 XX
 DT 20-MAY-1999 (first entry)
 XX
 DE KIAA0223 polymorphism in HA-1 negative homozygous individuals.
 XX
 KM T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
 KM transplant rejection; Graft-versus-Host disease; autoimmune disease;
 KM neoplastic haematopoietic cell; KIAA0223 polymorphism.
 XX
 OS Homo sapiens.
 XX
 XX WO9905173-A1.
 PN
 XX
 PD 04-FEB-1999.
 XX
 PF 23-JUL-1998; 98WO-NL000424.
 XX
 PR 23-JUL-1997; 97EP-00202303.
 XX
 PA (UYLE-) RIKKSUNIV LEIDEN.
 XX
 PI Goulmy EAJM, Hunt DF, Engelhard VH;
 XX
 DR WPI; 1999-142855/12.
 DR N-PSDB; AAX16080.
 XX
 PT Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
 PT for inducing tolerance to transplants and prevent rejection or graft-
 PT versus-host disease.
 XX
 XX Disclosure; Page 38; 57pp; English.
 PS
 CC The present sequence represents the KIAA0223 polymorphism in HA-1
 CC negative homozygous individuals. The specification describes an
 CC immunogenic peptide constituting a T-cell epitope, obtainable from the
 CC minor histocompatibility antigen HA-1. The peptide can be used in
 CC vaccines or pharmaceutical formulations as medicines to induce tolerance
 CC for transplants so as to prevent rejection and/or Graft-versus-Host
 CC disease, or to treat autoimmune diseases. Neoplastic haematopoietic cells
 CC presenting the peptides, in an HLA class I context, can be eliminated
 CC after specific recognition of the peptides. The peptides can also be used
 CC to raise antibodies, T-cell receptor, B- and T-cells

XX
 SQ Sequence 13 AA;
 Query Match 97.3%; Score 36; DB 2; Length 13;
 Best Local Similarity 88.9%; Pred. No. 1.8; 1; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 VLXDDLLEA 9
 |||||
 Db 3 VLHDDLLEA 11
 RESULT 13
 ABP71119
 ID ABP71119 standard; peptide; 10 AA.
 XX
 AC ABP71119;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE E10 protein CARD region fragment.
 XX
 KM BTF3; cell death; apoptosis; basic transcription factor; cyrostatic;
 KM neurotropic; neuroprotective; antiparkinsonian; antiarteriosclerotic;
 KM antirheumatic; antiarthritic; gene therapy; CARD; E10.
 XX
 OS Unidentified.
 XX
 XX WO200295001-A2.
 PN
 XX
 PD 28-NOV-2002.
 XX
 PF 21-MAY-2002; 2002MO-US016230.
 XX
 PR 21-MAY-2001; 2001US-0292559P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Rothman JH, Bloss T, Witze E;
 XX
 DR WPI; 2003-167228/16.
 XX
 XX
 PT Inhibiting or increasing programmed cell death of a cell, for treating
 PT e.g. cancer, comprises upregulating or inhibiting, respectively, the
 PT expression or activity of basic transcription factor (BTF)3 or its
 PT homolog in the cell.
 XX
 XX Example; Fig 2A; 84pp; English.
 PS
 CC The invention relates to inhibiting or increasing programmed cell death
 CC of a cell. The method involves upregulating or inhibiting, respectively,
 CC the expression or activity of basic transcription factor (BTF)3 or its
 CC homologue in the cell. The BTF3 polypeptides and nucleic acids are useful
 CC for inhibiting or increasing programmed cell death. They are used for
 CC screening for an agent that increases or inhibits programmed cell death
 CC or pre-screening for an agent that modulates programmed cell death, is used
 CC screened agent that increases or inhibits programmed diseases (e.g.
 CC for diagnosing or treating cancer or neurodegenerative diseases, Parkinson's disease
 CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease
 CC or multiple sclerosis), atherosclerosis, or rheumatoid arthritis.
 CC Sequences ABP71106-123 represent CARD regions of various CARD proteins
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 75.7%; Score 28; DB 6; Length 10;
 Best Local Similarity 85.7%; Pred. No. 57; 1; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 2 LXDDLLE 8
 |||||
 Db 3 LVDDLLE 9

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OM protein - protein search, using SW model

Run on: April 6, 2006, 16:57:26 ; Search time 19 Seconds
(without alignments)
45.576 Million cell updates/sec

Title: US-10-791-217A-1

Perfect score: 37

Sequence: 1 VLXDDLRA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	54.1	15	2	A53594
2	18	48.6	10	2	C26997
3	18	48.6	12	2	S39762
4	17	48.6	15	2	A26997
5	17	45.9	10	2	S13224
6	17	45.9	11	2	PH0924
7	17	45.9	13	2	PS0443
8	17	45.9	14	2	SS0900
9	17	45.9	14	2	C39170
10	17	45.9	15	2	B56819
11	17	45.9	15	2	S62675
12	16	43.2	7	2	S68004
13	16	43.2	8	2	PC4131
14	16	43.2	10	2	A61354
15	16	43.2	13	2	S14316
16	16	43.2	14	2	S29789
17	16	43.2	15	2	B32800
18	15	40.5	13	2	S12388
19	15	40.5	13	2	S65612
20	15	40.5	13	2	S00316
21	15	40.5	14	2	A61306
22	15	40.5	15	2	PQ0750
23	15	40.5	15	2	S29485
24	15	40.5	15	2	PH1788
25	15	40.5	15	2	D54226
26	14	37.8	7	2	S20446
27	14	37.8	7	2	A59489
28	14	37.8	10	2	F44644
29	14	37.8	10	2	E86128

30	14	37.8	11	2	PT0249	Ig heavy chain CRD
31	14	37.8	11	2	PH0922	T-cell receptor be
32	14	37.8	11	4	S41909	hypothetical prote
33	14	37.8	13	2	S41209	P420-non-reducing-
34	14	37.8	13	2	G44644	neurotoxin-associat
35	14	37.8	13	2	S01043	glutamate-ammonia
36	14	37.8	14	2	T46634	acyl carrier prote
37	14	37.8	14	2	PS0252	16K protein 5404 -
38	14	37.8	14	2	PH1626	Ig H chain V-D-J r
39	14	37.8	14	2	B61597	cytochrome P450 AL
40	14	37.8	14	2	IS1430	hemoglobin beta ch
41	14	37.8	15	2	PS0251	15K protein 5106 -
42	14	37.8	15	2	B26501	lipoprotein lipase
43	14	37.8	15	2	A26228	spot 42 protein -
44	14	37.8	15	2	PN0164	hycocyanine (6S)-d
45	14	37.8	15	2	A61522	7.5k surfactant-as

ALIGNMENTS

RESULT 1
A53594
calnexin - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C:Accession: A53594
R:Enter, M.; Vestweber, D.
J. Biol. Chem. 269, 12263-12268, 1994
A>Title: The integrin chains beta-1 and alpha-6 associate with the chaperone calnexin pr
A:Reference number: A53594; MUID:94216347; PMID:8163531
A:Accession: A53594
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <LEN>
A:Cross-references: UNIPROT:Q7M063; UNIPARC:UPI000017C62E
C:Keywords: endoplasmic reticulum; molecular chaperone

Query Match 54.1% Score 20; DB 2; Length 15;
Best Local Similarity 50.0% Pred. No. 5.4e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDL 6
DB 10 IIEDDL 15

RESULT 2

C26997
unspecific monooxygenase (EC 1.14.14.1) isozyme B, phenobarbital-inducible, hepatic - ra
N:Alternate names: cytochrome P450
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-2004
C:Accession: C26997
R:Graves, P.E.; Kaminsky, L.S.; Halpert, J.
Biochemistry 26, 3887-3894, 1987
A>Title: Evidence for functional and structural multiplicity of pregnenolone-16-alpha-ca
A:Reference number: A26997; MUID:8800604; PMID:3651420
A:Accession: C26997
A:Molecule type: protein
A:Residues: 1-10 <GRA>
A:Cross-references: UNIPROT:O06884; UNIPARC:UPI0000174DA8
C:Superfamily: cytochrome P450 homolog
C:Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembrane
Query Match 48.6% Score 18; DB 2; Length 10;
Best Local Similarity 80.0% Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DLEA 9
DB 2 DLEA 6

RESULT 3
S39762
cytochrome P450 17A1 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C:Accession: S39762
R:Ohishi, N.; Imada, S.; Suzuki, T.; Funae, Y.
Biochim. Biophys. Acta 1158, 227-236, 1993
A:Title: Characterization of two P-450 isozymes placed in the rat CYP2D subfamily.
A:Reference number: S39761; MUID:94072607; PMID:8251521
A:Accession: S39762
A:Molecule type: protein
A:Residues: 1-12 <OH>
A:Cross-references: UNIPARC:UPI000017C8F7

Query Match 48.6%; Score 18; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDL 6
DB 3 LIGDDL 8

RESULT 4
A26997
unspecific monooxygenase (EC 1.14.14.1) cytochrome P450 2B1, hepatic - rat (fragment)
N:Alternate names: cytochrome P450b
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-2004
C:Accession: A26997
R:Graves, P.E.; Kaminsky, L.S.; Halpert, J.
Biochemistry 26, 3887-3894, 1987
A:Title: Evidence for functional and structural multiplicity of pregnenolone-16-alpha-carboxylate monooxygenase
A:Reference number: A26997; MUID:88000604; PMID:3651420
A:Accession: A26997
A:Molecule type: protein
A:Residues: 1-15 <GRA>
A:Cross-references: UNIPROT:Q06884; UNIPARC:UPI0000174DA7
C:Superfamily: cytochrome P450 homology
C:Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembrane

Query Match 48.6%; Score 18; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DLLEA 9
DB 2 DLISA 6

RESULT 5
S13224
virg protein - Agrobacterium sp. (fragment)
C:Species: Agrobacterium sp.
C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C:Accession: S13224
R:Tamamoto, S.; Aoyama, T.; Takanami, M.; Oka, A.
J. Mol. Biol. 215, 537-547, 1990
A:Title: Binding of the regulatory protein VirG to the phased signal sequences upstream
A:Reference number: S13224; MUID:91039316; PMID:2231718
A:Accession: S13224
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <TRM>
A:Cross-references: UNIPROT:Q7M0P7; UNIPARC:UPI000017A9C4

Query Match 45.9%; Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDD 5

DB 6 VIDD 10

RESULT 6
PH0924
T-cell receptor beta chain V-D-J region (isolate 10) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1993 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0924
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A:Reference number: PH0924; MUID:92078857; PMID:1836012
A:Accession: PH0924
A:Molecule type: mRNA
A:Residues: 1-11 <GO>
A:Cross-references: UNIPARC:UPI000017C9F3
A:Experimental source: concanavalin A-activated lymphoblast
C:Keywords: T-cell receptor

Query Match 45.9%; Score 17; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DLLE 8
DB 7 DLME 10

RESULT 7
PS0443
potassium channel protein Slo G3 - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Feb-1997
C:Accession: PS0443
R:Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Bond
Neuron 9, 209-216, 1992
A:Title: Calcium-activated potassium channels expressed from cloned complementary DNAs.
A:Reference number: PS0443; MUID:92360298; PMID:1497890
A:Accession: PS0443
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-13 <ADE>
A:Cross-references: UNIPARC:UPI000017BEB4
C:Comment: This potassium channel is activated by calcium.
C:Genetics:
A:Gene: FlyBase:slo
A:Cross-references: FlyBase:FBgn003429
C:Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein

Query Match 45.9%; Score 17; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 7
DB 10 DDLV 13

RESULT 8
S50900
chlorophyll a/b-binding protein Lhcb5 - spinach (fragment)
N:Alternate names: light-harvesting complex LHCIIc protein
C:Species: Spinacia oleracea (spinach)
C:Date: 19-Mar-1997 #sequence_revision 23-Apr-1999 #text_change 23-Apr-1999
C:Accession: S50900
R:Walters, R.G.; Ruban, A.V.; Horton, P.
Eur. J. Biochem. 226, 1063-1069, 1994
A:Title: Higher plant light-harvesting complexes LHCIIa and LHCIIc are bound by dicyclo-
A:Reference number: S50900; MUID:95112835; PMID:7813461
A:Accession: S50900
A:Molecule type: protein

A:Residues: 1-14 <MAL>
 A:Cross-references: UNIPARC:UPI0000178182
 C:Superfamily: chlorophyll a/b-binding protein
 C:Keywords: chlorophyll; chloroplast; light-harvesting complex; photosynthesis; photoeye

Query Match 45.9%; Score 17; DB 2; Length 14;
 Best Local Similarity 57.1%; Pred. No. 2.1e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LXXDLE 8
 DB 3 LPDGLD 9

RESULT 9

C39170
 acyl-lacyl-carrier-protein] desaturase (EC 1.14.19.2) - avocado (fragments)
 C:Species: Persea americana (avocado)
 C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 03-Jun-2002
 C:Accession: C39170
 R:Shanklin, J.; Somerville, C.
 Proc. Natl. Acad. Sci. U.S.A. 88, 2510-2514, 1991
 A:Title: Stearoyl-acyl-carrier-protein desaturase from higher plants is structurally un
 A:Reference number: A39170; MUID:91172837; PMID:206187
 A:Accession: C39170
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <SHA>
 A:Cross-references: UNIPARC:UPI000017CD5B
 C:Keywords: oxidoreductase

Query Match 45.9%; Score 17; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DDLB 8
 DB 11 DILB 14

RESULT 10

B56819
 PS I complex subunit 8 - cucumber (fragment)
 C:Species: Cucumis sativus (cucumber)
 C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
 C:Accession: B56819
 R:Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.
 Biochim. Biophys. Acta 1059, 141-148, 1991
 A:Title: Characterization of genes that encode subunits of cucumber PS I complex by N-te
 A:Reference number: A56819; MUID:91355209; PMID:1883835
 A:Accession: B56819
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <IMA>
 A:Cross-references: UNIPROT:P42052; UNIPARC:UPI0000132593
 A:Note: sequence extracted from NCHI backbone (NCBIR:58606)

Query Match 45.9%; Score 17; DB 2; Length 15;
 Best Local Similarity 60.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXD 5
 DB 10 VLOD 14

RESULT 11

S62675
 collagen type I - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S62675
 R:Mizuno, M.; Kitafima, T.; Tomita, M.; Kuboki, Y.

Biochim. Biophys. Acta 1310, 97-102, 1996
 A:Title: The osteoblastic MC3T3-E1 cells synthesized C-terminal propeptide of type I col
 A:Reference number: S62675; MUID:97386332; PMID:9244181
 A:Accession: S62675
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <MIZ>
 A:Cross-references: UNIPROT:Q7M062; UNIPARC:UPI000017C63D

Query Match 45.9%; Score 17; DB 2; Length 15;
 Best Local Similarity 75.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DDLB 8
 DB 12 DILB 15

RESULT 12

S68004
 hucolin, 75K chain - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C:Accession: S68004
 R:Edgar, P.F.
 FEBS Lett. 375, 159-161, 1995
 A:Title: Hucolin, a new corticosteroid-binding protein from human plasma with structural
 A:Reference number: S68004; MUID:96087107; PMID:7498469
 A:Accession: S68004
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <EDG>
 A:Cross-references: UNIPARC:UPI000017C164

Query Match 43.2%; Score 16; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6
 DB 4 DDL 6

RESULT 13

PC4131
 hypothetical protein 8 [imported] - Pseudomonas aeruginosa (fragment)
 C:Species: Pseudomonas aeruginosa
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004
 C:Accession: PC4131
 R:Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.
 Gene 167, 87-91, 1995
 A:Title: Sequencing and characterization of the downstream region of the genes encoding
 Y for biosynthesis of heme d1.
 A:Reference number: J04552; MUID:96144254; PMID:8566817
 A:Accession: PC4131
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-8 <RAW>
 A:Cross-references: UNIPROT:P95412; UNIPARC:UPI000017A96A; DDBJ:D50473; NID:g1217594
 A:Note: this ORF is not annotated in Genbank entry PSEWIRC, release 113.0
 C:Superfamily: Pseudomonas stutzeri nird protein

Query Match 43.2%; Score 16; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6
 DB 2 DDL 4

RESULT 14

A61354

carnitine medium/long chain acyltransferase (EC 2.3.1.-) - rat (fragment)
N/Alternate names: endoplasmic reticulum protein ERp61; glucose regulated protein GRp58;
C/Species: Rattus norvegicus (Norway rat)
C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C/Accession: A61354
R/Murthy, M.S.R.; Pande, S.V.
Mol. Cell. Biochem. 122, 133-138, 1993
A/Title: Carnitine medium/long chain acyltransferase of microsomes seems to be the prev
A/Reference number: A61354; MUID:94049728; PMID:8232244
A/Accession: A61354
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <MUR>
A/Cross-references: UNIPARC:UPI000017C8DE
C/Keywords: acyltransferase

Query March 43.2%; Score 16; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DDLLE 8
|:|
Db 2 DYLE 5

RESULT 15

S14316
Photosystem I 9K chain - spinach (fragment)
C/Species: Spinacia oleracea (spinach)
C/Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C/Accession: S14316
R/Ikeuchl, M.; Inoue, Y.
FEBS Lett. 280, 332-334, 1991
A/Title: Two new components of 9 and 14 KDa from spinach photosystem I complex.
A/Reference number: S14316; MUID:91192162; PMID:2013332
A/Accession: S14316
A/Molecule type: protein
A/Residues: 1-13 <IKE>
A/Cross-references: UNIPROT:Q7MLJ1; UNIPARC:UPI000017AF28
C/Keywords: membrane-associated complex; photosynthesis; photosystem I

Query March 43.2%; Score 16; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DDLLE 8
|:|
Db 4 DYLE 8

Search completed: April 6, 2006, 17:03:58
Job time : 20 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 6, 2006, 16:51:26 ; Search time 116.333 Seconds
(without alignments)
54.582 Million cell updates/sec

Title: US-10-791-217a-1
Perfect score: 37
Sequence: 1 VLXDDLRA 9

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 7855

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	56.8	11	1	UPF05_MOUSE
2	21	56.8	13	2	P82560_STRPY
3	20	54.1	15	2	Q7M063_MOUSE
4	19	51.4	11	2	Q47600_ECOLI
5	19	51.4	15	2	Q9UC60_HUMAN
6	19	51.4	15	2	Q9RS06_CHRVI
7	18	48.6	10	2	Q718N9_PPAPA
8	18	48.6	11	2	Q9QVC5_RAT
9	18	48.6	11	2	Q718K6_PPAPA
10	18	48.6	12	1	X1YA_STRVA
11	18	48.6	12	2	Q9RT03_BOVIN
12	18	48.6	12	2	Q9TOY4_BOVIN
13	18	48.6	12	2	Q5MK49_9CLOS
14	18	48.6	12	2	Q5MK52_9CLOS
15	18	48.6	12	2	Q5MK66_9CLOS
16	18	48.6	12	2	Q5MK81_9CLOS
17	18	48.6	13	1	TE1JA_RANJA
18	18	48.6	13	2	Q8WYB7_HUMAN
19	18	48.6	13	2	Q7TE19_9CLOS
20	18	48.6	13	2	Q7TE20_9CLOS
21	18	48.6	13	2	Q7TE22_9CLOS
22	18	48.6	13	2	Q7TE26_9CLOS
23	18	48.6	13	2	Q7TE30_9CLOS
24	18	48.6	14	2	Q68CX5_HUMAN
25	18	48.6	14	2	Q52B40_RHIL0
26	18	48.6	14	2	Q92B42_STRPY
27	17	45.9	10	2	Q9UMMS_SULSO
28	17	45.9	10	2	Q5S733_SFUNG
29	17	45.9	10	2	Q5S733_SFUNG
30	17	45.9	10	2	Q9TOVA_HORSE
31	17	45.9	10	2	Q7M0P7_AGRSP

ALIGNMENTS

RESULT 1	ID	UPF05_MOUSE	STANDARD	PRT	11 AA.
AC	P38643;				
DT	01-OCT-1994 (Rel. 30, Created)				
DT	01-OCT-1994 (Rel. 30, Last sequence update)				
DT	05-JUL-2004 (Rel. 44, Last annotation update)				
DE	Unknown protein from 2D-PAGE of fibroblasts (P48) (Fragment).				
OS	Mus musculus (Mouse).				
OC	Karyotype; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;				
OC	Muridae; Muridae; Murinae; Mus.				
OX	NCBI_TaxId=10090;				
RN	[1]				
RP	PROTEIN SEQUENCE.				
RC	TISSUE=Fibroblast;				
RA	MEDLINE=9500907; PubMed=7523108;				
RX	Merrick B.A., Patterson R.M., Wichter L.J., He C., Selkirk J.K.;				
RT	"Separation and sequencing of familial and novel murine proteins using				
RL	Electrophoresis 15:735-745(1994)."				
CC	-1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown				
CC	protein is: 5.5, its MW is: 48 kDa.				
CC					
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use as long as its content is in no way modified and this statement is not				
CC	removed.				
KW	Direct protein sequencing.				
FT	NON_TER				
FT	SEQUENCE 11 AA; 1330 MW; E54835E5CAABAPA CRG64;				

Query Match 56.8%; Score 21; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLRA 8
:||||:
DB 3 IXXDDVIE 10

RESULT 2
P82560_STRPY PRELIMINARY; PRT; 13 AA.
ID P82560;
AC P82560;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.

```

OX NCBI_TaxID=1314;
RN [1]
RP PROTEIN SEQUENCE. AND MASS SPECTROMETRY.
RC STRAIN=JRS4;
RA Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
  Vanbogelen R.A.; gel electrophoresis map of Streptococcus pyogenes
RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
  proteins."
RL Submitted (MAY-2000) to Swiss-Prot.
CC -1- MASS SPECTROMETRY; MW=30142.85; METHOD=Electrospray.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1464 MW; CPE7BD129CB0C6D9 CRC64;

Query Match
Best Local Similarity 56.8%; Score 21; DB 2; Length 13;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 LKXDLLEA 9
Db 1 ITDVFQOA 8

RESULT 3
Q7M063_MOUSE PRELIMINARY; PRT; 15 AA.
ID Q7M063_MOUSE PRELIMINARY; PRT; 15 AA.
AC Q7M063;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Calnexin (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
  Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=94216347; PubMed=8163531;
RA Lenter M., Vestweber D.;
RT "The integrin chains beta-1 and alpha-6 associate with the chaperone
  calnexin prior to integrin assembly."
RL J. Biol. Chem. 269:12263-12268(1994).
DR PIR; A53594; A53594.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1693 MW; C62AAAA42P9F5F35 CRC64;

Query Match
Best Local Similarity 54.1%; Score 20; DB 2; Length 15;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLKXDL 6
Db 10 IIRDDL 15

RESULT 4
Q47600_ECOLI PRELIMINARY; PRT; 11 AA.
ID Q47600_ECOLI PRELIMINARY; PRT; 11 AA.
AC Q47600;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribase protein (Fragment).
OS Name=Ribase;
  Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91139577; PubMed=1995588;

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RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
  modification systems."
RL J. Bacteriol. 173:1367-1375 (1991).
DR EMBL; M63619; AAA24556.1; -; Genomic_DNA.
FT NON_TER 11 11
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1232 MW; 63175479572ABS5A4 CRC64;

Query Match
Best Local Similarity 51.4%; Score 19; DB 2; Length 11;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 LKXDLLEA 9
Db 3 LRSDLINA 10

RESULT 5
Q9UC60_HUMAN PRELIMINARY; PRT; 15 AA.
ID Q9UC60_HUMAN PRELIMINARY; PRT; 15 AA.
AC Q9UC60;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE N-acetylmuramyl-L-alanine amidase (EC 3.5.1.28) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
  Homo.
NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95392215; PubMed=7663175; DOI=10.1006/prep.1995.1049;
RA De Pauw P., Neyt C., Vandewinkel B., Wattiez R., Palagne P.;
RT "Characterization of human serum N-acetylmuramyl-L-alanine amidase
  purified by affinity chromatography."
RL Protein Expr. Purif. 6:371-378(1995).
DR GO; GO:0008745; P:peptide amidation; NAS.
DR GO; GO:0001519; P:peptide amidation; NAS.
SQ SEQUENCE 15 AA; 1600 MW; 9016B00FF9E780A CRC64;

Query Match
Best Local Similarity 51.4%; Score 19; DB 2; Length 15;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 VLKXDLLEA 9
Db 4 LMDSVIOA 12

RESULT 6
Q9R5D6_CHRVI PRELIMINARY; PRT; 15 AA.
ID Q9R5D6_CHRVI PRELIMINARY; PRT; 15 AA.
AC Q9R5D6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE POLY(3-HYDROXYBUTYRIC acid) granule-associated 41 kDa protein
  (Fragment).
OS Chromatium vinosum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
  Chromatiaceae; Allochromatium.
NCBI_TaxID=1049;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93146381; PubMed=1490603; DOI=10.1016/0378-1097(92)90031-I;
RA Iiebergseil M., Schmidt B., Steinbuechel A.;
RT "Isolation and identification of granule-associated proteins relevant
  for poly(3-hydroxyalkanoic acid) biosynthesis in Chromatium vinosum
  D."
RL FEMS Microbiol. Lett. 78:227-232(1992).
SQ SEQUENCE 15 AA; 1874 MW; 165FA9A16BCA2A9D CRC64;

```

Query Match 51.4%; Score 19; DB 2; Length 15;
 Best Local Similarity 80.0%; Pred. No. 8.3e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 DDLLR 8
 DB 9 DDMLR 13

RESULT 7

Q718N9_9PARA PRELIMINARY; PRT; 10 AA.
 AC Q718N9;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hemagglutinin-neuraminidase (Fragment).
 OS Newcastle disease virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Avulaviruses.
 NCBI_TaxID=11176;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Gould A.R., Hansson B., Selleck K., Kattenbelt J.A., Mackenzie M.,
 RA Della-Porta A.J.;
 RT "Newcastle disease virus fusion and hemagglutinin-neuraminidase gene
 RT motifs as markers for viral lineage.";
 RL Avian Pathol. 32:361-373(2003).
 DR EMBL; AF542884; AAQ11609.1; -; Genomic_DNA.
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1100 MW; 711806AAA337205B CRC64;

Query Match 48.6%; Score 18; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 8.7e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDD 5
 DB 4 ILKDD 8

RESULT 8

Q9QVC5_RAT PRELIMINARY; PRT; 11 AA.
 AC Q9QVC5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE DM53 protein (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA MEDLINE=92291078; PubMed=1601872;
 RA Sudarmaniam V.N., Bin Mohd Yusoff A.R., Wong S.H., Lim G.B., Chew M.,
 RA Hong W.;
 RT "Biochemical fractionation and characterization of proteins from
 RT Golgi-enriched membranes.";
 RL J. Biol. Chem. 267:12016-12021(1992).
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1210 MW; 5B61C10B9DADB2C7 CRC64;

Query Match 48.6%; Score 18; DB 2; Length 11;
 Best Local Similarity 44.4%; Pred. No. 9.7e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VLXDDLEA 9
 DB 3 VLVDAMLHS 11

RESULT 9
 Q718K6_9PARA PRELIMINARY; PRT; 11 AA.
 AC Q718K6;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hemagglutinin-neuraminidase (Fragment).
 OS Newcastle disease virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Avulaviruses.
 NCBI_TaxID=11176;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Gould A.R., Hansson B., Selleck K., Kattenbelt J.A., Mackenzie M.,
 RA Della-Porta A.J.;
 RT "Newcastle disease virus fusion and hemagglutinin-neuraminidase gene
 RT motifs as markers for viral lineage.";
 RL Avian Pathol. 32:361-373(2003).
 DR EMBL; AF542917; AAQ11642.1; -; Genomic_DNA.
 FT NON_TER 1
 SQ SEQUENCE 11 AA; 1313 MW; 710428D6A337205B CRC64;

Query Match 48.6%; Score 18; DB 2; Length 11;
 Best Local Similarity 60.0%; Pred. No. 9.7e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDD 5
 DB 5 ILKDD 9

RESULT 10

XYLA_STRVN STANDARD; PRT; 12 AA.
 AC P14405;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Xylose isomerase (EC 5.3.1.5) (Fragment).
 GN Name=xy1A;
 OS Streptomyces violaceoruber.
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Streptomycetaceae; Streptomycetaceae; Streptomycetes.
 NCBI_TaxID=1935;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA STRAIN=LMG 7183;
 RX MEDLINE=90104230; PubMed=2604694;
 RA Vangryperre W., Ampe C., Kersters-Hilderson H., Tempet P.;
 RT "Single active-site histidine in D-xylose isomerase from Streptomyces
 RT violaceoruber. Identification by chemical derivatization and peptide
 RT mapping.";
 RL Biochem. J. 263:195-199(1989).
 CC -1- CATALYTIC ACTIVITY: D-xylose = D-xylulose.
 CC -1- COFACTOR: Binds 2 magnesium ions per subunit (Potential).
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to the xylose isomerase family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC HAAP, MF 00455; -, 1.
 DR InterPro; IPR001998; Xylose_isom.
 DR PROSITE; PS00172; XYLOSE_ISOMERASE_1; PARTIAL.
 DR PROSITE; PS00173; XYLOSE_ISOMERASE_2; PARTIAL.
 KW Carbohydrate metabolism; Direct protein sequencing; Isomerase;
 KW Magnesium; Metal-binding; Pentose shunt; Xylose metabolism.

FT ACT_SITE 5 5
 FT ACT_SITE 8 8 By similarity.
 FT NON_TER 1 1
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA, 1376 MW, E749268BBI1AAAA1 CRC64;

Query March 48.6%; Score 18; DB 1; Length 12;
 Best Local Similarity 75.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 DDL 7
 |||:
 7 DDL 10

RESULT 11
 Q9T2U3 BOVIN PRELIMINARY; PRT; 12 AA.
 AC Q9T2U3-

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE NAH:ubiquinone oxidoreductase (Complex I) iron-sulfur protein
 DE fraction 20 kDa polypeptide peptide T-8 (Fragment).
 OS Bos taurus (Bovine).

OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;

RN [1]

RP PROTEIN SEQUENCE.
 RX MEDLINE=92138662; PubMed=1778979;

RA Masui R., Wakabayashi S., Matsubara H., Hatefi Y.,
 RT "The amino acid sequence of the 9 kDa polypeptide and partial amino
 RT acid sequence of the 20 kDa polypeptide of mitochondrial
 RL NAH:ubiquinone oxidoreductase.";
 RL J. Biochem. 110:575-582(1991).

FT NON_TER 1 1
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA, 1335 MW, CC9702EC3C233DC2 CRC64;

Query Match 48.6%; Score 18; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 DDL 7
 |||:
 9 DDL 12

RESULT 12
 Q9TOY4 BOVIN PRELIMINARY; PRT; 12 AA.
 AC Q9TOY4-

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Glycoprotein H-B N-TERMINAL, GPB-B N-TERMINAL=KEX2/subtilisin-related
 DE protease (Fragment).
 OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=91340701; PubMed=1874725;

RA Christie D.L., Batchelor D.C., Palmer D.U.;
 RT "Identification of kex2-related proteases in chromaffin granules by
 RT partial amino acid sequence analysis.";
 RL J. Biol. Chem. 266:15679-15683(1991).

FT NON_TER 1 1

FT NON_TER 12 12
 SQ SEQUENCE 12 AA, 1303 MW, 9F2FF9E2782DC5BA CRC64;

Query Match 48.6%; Score 18; DB 2; Length 12;
 Best Local Similarity 62.5%; Pred. No. 1.1e+04;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VLXDDLE 8
 |||:
 2 VLXDSALD 9

RESULT 13
 Q5MK49 9CLOS PRELIMINARY; PRT; 12 AA.
 AC Q5MK49-

DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DE RdRp (Fragment).
 OS Citrus tristata virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
 OC Closterovirus.
 OC NCBI_TaxID=12162;

RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=B359;

RA Hilf M.B., Mavrodieva V.A., Garnsey S.M.;
 RT "POL and K17 markers from Beltsville CTV isolates.";
 RT Submitted (SEP-2004) to the EMBL/Genbank/DBJ databases.

DR EMBL; AY756309; AAW22818.1; -; Genomic_RNA.

FT NON_TER 1 1
 SQ SEQUENCE 12 AA, 1146 MW, CAA485D77F187DC6 CRC64;

Query Match 48.6%; Score 18; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 1.1e+04;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 DDL 9
 |||:
 1 DDL 6

RESULT 14
 Q5MK52 9CLOS PRELIMINARY; PRT; 12 AA.
 AC Q5MK52-

DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)

DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE RdRp (Fragment).

OS Citrus tristata virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
 OC Closterovirus.
 OC NCBI_TaxID=12162;

RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=B358;

RA Hilf M.B., Mavrodieva V.A., Garnsey S.M.;
 RT "POL and K17 markers from Beltsville CTV isolates.";
 RT Submitted (SEP-2004) to the EMBL/Genbank/DBJ databases.

DR EMBL; AY756307; AAW22815.1; -; Genomic_RNA.

FT NON_TER 1 1
 SQ SEQUENCE 12 AA, 1146 MW, CAA485D77F187DC6 CRC64;

Query Match 48.6%; Score 18; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 1.1e+04;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 DDL 9
 |||:
 1 DDL 6

```

RESULT 15
OSMK66_9CLOS PRELIMINARY; PRT; 12 AA.
ID OSMK66_9CLOS
AC OSMK66_
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE RdRp (Fragment).
OS Citrus tristezza virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Closterovirus.
OX NCBI_TaxID=12162;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B183;
RA Hilf M.E., Mavrodieva V.A., Garnsey S.M.;
RT "POL and K17 markers from Beltsville CTV isolates.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY756294; AAW22796.1; -; Genomic_RNA.
FT NON TER 1
SQ SEQUENCE 12 AA; 1146 MW; CAA485D77F187DC6 CRC64;

Query Match 48.6%; Score 18; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DDLLEA 9
   |||:|
   1 DDLGQA 6

Db

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Search completed: April 6, 2006, 17:02:57
 Job time : 119.333 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 6, 2006, 17:03:16 ; Search time 27.6667 Seconds
(without alignments)
26.894 Million cell updates/sec

Title: US-10-791-217A-1

Perfect score: 37

Sequence: 1 VLXDDLRA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 186887

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCITUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	97.3	9	2	US-09-269-250E-18
2	36	97.3	9	2	US-09-269-250E-20
3	36	97.3	9	2	US-09-269-250E-29
4	36	97.3	9	2	US-09-489-760-1
5	36	97.3	9	2	US-09-489-760-2
6	36	97.3	9	2	US-09-489-760-5
7	36	97.3	13	2	US-09-269-250E-26
8	36	97.3	13	2	US-09-269-250E-28
9	36	97.3	13	2	US-09-489-760-14
10	36	97.3	13	2	US-09-489-760-16
11	23	62.2	8	2	US-09-269-250E-38
12	23	62.2	15	2	US-08-940-095-104
13	23	62.2	15	2	US-08-940-093-104
14	23	62.2	15	2	US-08-940-096-104
15	23	62.2	15	2	US-09-465-719-104
16	23	62.2	15	2	US-09-453-605-104
17	23	62.2	15	2	US-09-453-838-104
18	23	62.2	15	2	US-08-940-136-104
19	23	62.2	15	2	US-09-453-841-104
20	23	62.2	15	2	US-09-453-833-104
21	23	62.2	15	2	US-09-453-826-104
22	23	62.2	15	2	US-09-453-840-104
23	23	62.2	15	2	US-09-865-989-104
24	23	62.2	15	2	US-09-453-834-104
25	23	62.2	15	2	US-10-283-599-104
26	23	62.2	15	2	US-09-465-718-104
27	22	59.5	7	2	US-08-556-419-14

28	22	59.5	9	2	US-09-744-549-15	Sequence 15, App1
29	22	59.5	9	2	US-10-394-980-421	Sequence 421, App
30	22	59.5	9	2	US-10-394-980-464	Sequence 464, App
31	22	59.5	11	1	US-08-726-136-13	Sequence 13, App1
32	22	59.5	11	2	US-09-103-434-13	Sequence 13, App1
33	22	59.5	11	2	US-09-687-594-13	Sequence 13, App1
34	22	59.5	12	2	US-09-569-037-1	Sequence 1, App1
35	22	59.5	14	1	US-08-366-276-9	Sequence 9, App1
36	22	59.5	15	2	US-09-069-827A-132	Sequence 132, App
37	22	59.5	15	2	US-09-050-733-79	Sequence 79, App1
38	21	56.8	6	1	US-08-459-568-20	Sequence 20, App1
39	21	56.8	6	1	US-08-399-411-20	Sequence 20, App1
40	21	56.8	6	2	US-08-516-859A-20	Sequence 20, App1
41	21	56.8	6	2	US-09-586-472-20	Sequence 20, App1
42	21	56.8	6	2	US-09-528-706-20	Sequence 20, App1
43	21	56.8	6	1	US-08-459-568-75	Sequence 75, App1
44	21	56.8	8	1	US-08-399-411-75	Sequence 75, App1
45	21	56.8	8	2	US-08-516-859A-75	Sequence 75, App1

ALIGNMENTS

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RESULT 1
US-09-269-250E-18
; Sequence 18, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elia
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-18

Query Match      97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches      8; Conservative      0; Mismatches      1; Indels      0;

Qy      1 VLXDDLRA 9
Db      1 VLXDDLRA 9

RESULT 2
US-09-269-250E-20
; Sequence 20, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elia
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-20

Query Match      97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches      8; Conservative      0; Mismatches      1; Indels      0;
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Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
|||
1 VLHDDLLEA 9

RESULT 3

US-09-269-250E-29
; Sequence 29, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elise
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (3)-(3)
; OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
US-09-269-250E-29

Query Match 97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
|||
1 VLHDDLLEA 9

RESULT 4

US-09-489-760-1
; Sequence 1, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leiden
; APPLICANT: Goulmy, Elise A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Histocompatibility antigen
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (3)
; OTHER INFORMATION: AMINO ACID X REPRESENTS A HISTIDINE OR AN ARGININE
; OTHER INFORMATION: RESIDUE
US-09-489-760-1

Query Match 97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
|||
1 VLHDDLLEA 9

Db 1 VLXDDLLEA 9

RESULT 5

US-09-489-760-2
; Sequence 2, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leiden
; APPLICANT: Goulmy, Elise A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Histocompatibility antigen
US-09-489-760-2

Query Match 97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
|||
1 VLHDDLLEA 9

RESULT 6

US-09-489-760-5
; Sequence 5, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leiden
; APPLICANT: Goulmy, Elise A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: KIAA0223 partial complementary DNA
US-09-489-760-5

Query Match 97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
|||
1 VLHDDLLEA 9

RESULT 7

US-09-269-250E-26
; Sequence 26, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elise


```

; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Product
US-09-269-250E-26

Query Match
Best Local Similarity 97.3%; Score 36; DB 2; Length 13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
   |||||
Db 3 VLHDDLLEA 11

RESULT 8
US-09-269-250E-28
; Sequence 28, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 28
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Product
US-09-269-250E-28

Query Match
Best Local Similarity 97.3%; Score 36; DB 2; Length 13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
   |||||
Db 3 VLHDDLLEA 11

RESULT 9
US-09-489-760-14
; Sequence 14, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leiden
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown Organism

```

```

; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:HA-1-/-
US-09-489-760-14

Query Match
Best Local Similarity 97.3%; Score 36; DB 2; Length 13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
   |||||
Db 3 VLHDDLLEA 11

RESULT 10
US-09-489-760-16
; Sequence 16, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leiden
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:HA-1/+
US-09-489-760-16

Query Match
Best Local Similarity 97.3%; Score 36; DB 2; Length 13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
   |||||
Db 3 VLHDDLLEA 11

RESULT 11
US-09-269-250E-38
; Sequence 38, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 38
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN
US-09-269-250E-38

Query Match
Best Local Similarity 62.2%; Score 23; DB 2; Length 8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DLLEA 9
   |||||
Db 4 DLLEA 8

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RESULT 12
US-08-940-095-104
Sequence 104, Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6004925e
US-08-940-095-104
Query Match 62.2%; Score 23; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 LKXDLLEA 9
| : : : : :
| : : : : :
DB 2 LKXDLLEA 9
RESULT 13
US-08-940-093-104
Sequence 104, Application US/08940093
Patent No. 6037323
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,093
FILING DATE: 29-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6037323e
US-08-940-093-104
Query Match 62.2%; Score 23; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 LKXDLLEA 9
| : : : : :
| : : : : :
DB 2 LKXDLLEA 9
RESULT 14
US-08-940-096-104
Sequence 104, Application US/08940096
Patent No. 6046166
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6046166e
US-08-940-096-104

Query Match
Best Local Similarity 62.2%; Score 23; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKDDLLEA 9
DB 2 LKDDLLEA 9

RESULT 15
US-09-465-719-104
Sequence 104, Application US/09465719
Patent No. 6265377
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,719
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,093
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6265377e
US-09-465-719-104

Query Match
Best Local Similarity 62.2%; Score 23; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKDDLLEA 9
DB 2 LKDDLLEA 9

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Job time : 27.6667 secs

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OM protein - protein search, using sw model

Run on: April 6, 2006, 17:22:22 ; Search time 96.6667 Seconds
(without alignments)
38.901 Million cell updates/sec

Title: US-10-791-217A-1
Perfect score: 37
Sequence: 1 VLXDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 324073

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	36	97.3	9	4	US-10-623-176-2
3	36	97.3	9	4	US-10-623-176-10
4	36	97.3	9	4	US-10-791-217-1
5	36	97.3	9	4	US-10-791-217-2
6	36	97.3	9	4	US-10-791-217-5
7	36	97.3	9	5	US-10-861-335-1
8	36	97.3	9	6	US-11-007-740-18
9	36	97.3	9	6	US-11-007-740-20
10	36	97.3	9	6	US-11-007-740-29
11	36	97.3	10	4	US-10-623-176-24
12	36	97.3	10	4	US-10-623-176-43
13	36	97.3	10	4	US-10-623-176-44
14	36	97.3	12	4	US-10-623-176-65
15	36	97.3	13	4	US-10-623-176-74
16	36	97.3	13	4	US-10-623-176-76
17	36	97.3	13	4	US-10-791-217-14
18	36	97.3	13	4	US-10-791-217-16
19	36	97.3	13	6	US-11-007-740-26
20	36	97.3	13	6	US-11-007-740-28
21	32	86.5	9	4	US-10-623-176-41
22	32	86.5	9	4	US-10-623-176-42
23	32	86.5	9	4	US-10-623-176-45
24	32	86.5	9	4	US-10-623-176-46
25	29	78.4	9	4	US-10-623-176-47
26	29	78.4	9	4	US-10-623-176-48
27	28	75.7	10	4	US-10-153-344-11

28	27	73.0	9	4	US-10-623-176-23	Sequence 23, Appl
29	27	73.0	9	4	US-10-623-176-40	Sequence 40, Appl
30	27	73.0	10	4	US-10-623-176-6	Sequence 6, Appl
31	27	73.0	10	4	US-10-623-176-7	Sequence 7, Appl
32	27	73.0	10	4	US-10-623-176-8	Sequence 8, Appl
33	27	73.0	13	4	US-10-623-176-54	Sequence 54, Appl
34	27	73.0	13	4	US-10-623-176-64	Sequence 64, Appl
35	25	67.6	10	3	US-09-572-404B-428	Sequence 428, Appl
36	25	67.6	10	4	US-10-702-400-90	Sequence 90, Appl
37	25	67.6	10	5	US-10-805-650-90	Sequence 90, Appl
38	25	67.6	13	4	US-10-468-496-761	Sequence 761, Appl
39	25	67.6	13	4	US-10-468-496-762	Sequence 762, Appl
40	25	67.6	13	4	US-10-468-496-763	Sequence 763, Appl
41	25	67.6	13	4	US-10-468-496-764	Sequence 764, Appl
42	24	64.9	10	5	US-10-773-274A-7	Sequence 7, Appl
43	24	64.9	13	4	US-10-145-415-66	Sequence 66, Appl
44	23	62.2	8	4	US-10-623-176-15	Sequence 15, Appl
45	23	62.2	8	6	US-11-007-740-38	Sequence 38, Appl

ALIGNMENTS

```
RESULT 1
US-10-623-176-1
; Sequence 1, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-604705
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-1

Query Match          97.3%; Score 36; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLXDLLEA 9
Db      1 VLXDLLEA 9

RESULT 2
US-10-623-176-2
; Sequence 2, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
```

APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(9)
US-10-623-176-2

Query Match 97.3%; Score 36; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0;

QY 1 VLXDDLLEA 9
|||
1 VLHDDLLEA 9

RESULT 3
US-10-623-176-10
Sequence 10, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Elsa A.J.M.
APPLICANT: Hunt, Donald P.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(9)
US-10-623-176-10

Query Match 97.3%; Score 36; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9

Db |||
1 VLHDDLLEA 9

RESULT 4
US-10-791-217-1
Sequence 1, Application US/10791217
Publication No. US20040191268A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Elsa A.J.M.
APPLICANT: Hunt, Donald P.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: The HA-1 Antigen
FILE REFERENCE: 2183-4285US
CURRENT APPLICATION NUMBER: US/10/791,217
CURRENT FILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: US/09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: obtained from histocompatibility antigen
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (3)..(3)
OTHER INFORMATION: Xaa is HISTIDINE OR ARGININE RESIDUE
US-10-791-217-1

Query Match 97.3%; Score 36; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
|||
1 VLXDDLLEA 9

RESULT 5
US-10-791-217-2
Sequence 2, Application US/10791217
Publication No. US20040191268A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Elsa A.J.M.
APPLICANT: Hunt, Donald P.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: The HA-1 Antigen
FILE REFERENCE: 2183-4285US
CURRENT APPLICATION NUMBER: US/10/791,217
CURRENT FILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: US/09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: obtained from histocompatibility antigen
US-10-791-217-2

Query Match 97.3%; Score 36; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLXDDLLEA 9
|||
Db 1 VLHDDLLEA 9

RESULT 6

US-10-791-217-5
; Sequence 5, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Elia A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Engelhard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/10/791,217
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: obtained from KIAA0223 partial complementary DNA
US-10-791-217-5

Query Match 97.3%; Score 36; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLXDDLLEA 9
|||
Db 1 VLHDDLLEA 9

RESULT 7

US-10-861-335-1
; Sequence 1, Application US/10861335
; Publication No. US20050031612A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Elia A.J.M.
; TITLE OF INVENTION: Minor histocompatibility antigen HA-1: target antigen for immunot
; TITLE OF INVENTION: Of tumors
; FILE REFERENCE: 2183-6479US
; CURRENT APPLICATION NUMBER: US/10/861,335
; PRIOR APPLICATION NUMBER: PCT/NL02/00791
; PRIOR FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: EP 01204704.9
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HA-1 peptide
US-10-861-335-1

Query Match 97.3%; Score 36; DB 5; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLXDDLLEA 9
|||
Db 1 VLHDDLLEA 9

RESULT 8

US-11-007-740-18
; Sequence 18, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Elia
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 2799/58994-A
; CURRENT APPLICATION NUMBER: US/11/007,740
; CURRENT FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: 09/269,250
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-18

Query Match 97.3%; Score 36; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLXDDLLEA 9
|||
Db 1 VLHDDLLEA 9

RESULT 9

US-11-007-740-20
; Sequence 20, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Elia
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 2799/58994-A
; CURRENT APPLICATION NUMBER: US/11/007,740
; CURRENT FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: 09/269,250
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-20

Query Match 97.3%; Score 36; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLXDDLLEA 9
|||
Db 1 VLHDDLLEA 9

RESULT 10

US-11-007-740-29
; Sequence 29, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Elia
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 2799/58994-A
; CURRENT APPLICATION NUMBER: US/11/007,740
; CURRENT FILING DATE: 2004-12-08

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;; PRIOR APPLICATION NUMBER: 09/269,250
;; PRIOR FILING DATE: 1999-05-21
;; NUMBER OF SEQ ID NOS: 40
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 29
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (3)..(3)
;; OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
US-11-007-740-29
```

```
Query Match          97.3%; Score 36; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 VLXDDLLEA 9
Db      1 VLXDDLLEA 9
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RESULT 11
US-10-623-176-24
; Sequence 24, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
```

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; APPLICANT: Goulimy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; OTHER INFORMATION: wherein X can be H or R
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(10)
US-10-623-176-24
```

US-10-623-176-24

```
Query Match          97.3%; Score 36; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 VLXDDLLEA 9
Db      1 VLXDDLLEA 9
```

RESULT 12

```
US-10-623-176-43
; Sequence 43, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
```

```
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: (1)..(10)
US-10-623-176-43
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```
Query Match          97.3%; Score 36; DB 4; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
Qy      1 VLXDDLLEA 9
Db      1 VLXDDLLEA 9
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RESULT 13

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US-10-623-176-44
; Sequence 44, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: (1)..(10)
US-10-623-176-44
```

```
Query Match          97.3%; Score 36; DB 4; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
Qy      1 VLXDDLLEA 9
```


Db 1 VLXDDLLEA 9
RESULT 14
US-10-623-176-65
; Sequence 65, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elb A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: (1)..(12)
US-10-623-176-65
Query Match 97.3%; Score 36; DB 4; Length 12;
Best Local Similarity 88.9%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 VLXDDLLEA 9
Db 2 VLXDDLLEA 10
RESULT 15
US-10-623-176-74
; Sequence 74, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elb A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: KIAA0223
; OTHER INFORMATION: sequence derived from a presumed HA-1 negative
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(13)
US-10-623-176-74
Query Match 97.3%; Score 36; DB 4; Length 13;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 VLXDDLLEA 9
Db 3 VLXDDLLEA 11
Search completed: April 6, 2006, 17:28:45
Job time : 97.6667 secs

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OM protein - protein search, using SW model

Run on: April 6, 2006, 17:24:07 ; Search time 12.6667 Seconds
(without alignments)
22.163 Million cell updates/sec

Title: US-10-791-217A-1

Perfect score: 37

Sequence: 1 VLXDDLLEA 9

Scoring table: BIOSUM62

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Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 65691

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Maximum DB seq length: 15

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Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	97.3	9	US-11-010-748A-11	Sequence 11, Appl
2	36	97.3	9	US-11-010-748A-12	Sequence 12, Appl
3	22	59.5	15	US-11-172-740-1404	Sequence 1404, Ap
4	21	56.8	9	US-10-927-435-63	Sequence 63, Appl
5	21	56.8	9	US-10-927-634-63	Sequence 63, Appl
6	21	56.8	15	US-10-353-783-71	Sequence 71, Appl
7	20	54.1	5	US-11-129-143-168	Sequence 168, App
8	20	54.1	5	US-11-129-143-168	Sequence 168, App
9	20	54.1	5	US-11-129-143-170	Sequence 170, App
10	20	54.1	5	US-11-129-143-171	Sequence 171, App
11	20	54.1	5	US-11-129-143-172	Sequence 172, App
12	20	54.1	5	US-11-129-143-173	Sequence 173, App
13	20	54.1	7	US-10-982-440-126	Sequence 126, App
14	20	54.1	8	US-11-021-305-62	Sequence 62, Appl
15	20	54.1	8	US-11-021-305-62	Sequence 62, Appl
16	20	54.1	8	US-11-021-305-65	Sequence 65, Appl
17	20	54.1	10	US-10-989-767A-159	Sequence 66, Appl
18	20	54.1	10	US-10-989-767A-159	Sequence 66, Appl
19	20	54.1	10	US-10-989-767A-441	Sequence 441, App
20	20	54.1	12	US-11-004-399-1909	Sequence 547, App
21	20	54.1	13	US-11-207-078-102	Sequence 102, App
22	19	51.4	6	US-11-207-078-373	Sequence 373, App
23	19	51.4	7	US-11-225-686-2954	Sequence 2954, Ap
24	19	51.4	7	US-11-225-686-3877	Sequence 3877, Ap
25	19	51.4	7	US-11-225-686-3914	Sequence 3914, Ap

26	19	51.4	7	US-11-225-686-3915	Sequence 3915, Ap
27	19	51.4	7	US-11-225-686-3916	Sequence 3916, Ap
28	19	51.4	7	US-11-225-686-3932	Sequence 3932, Ap
29	19	51.4	7	US-11-225-686-3941	Sequence 3941, Ap
30	19	51.4	7	US-11-202-009-2954	Sequence 2954, Ap
31	19	51.4	7	US-11-202-009-3877	Sequence 3877, Ap
32	19	51.4	7	US-11-202-009-3914	Sequence 3914, Ap
33	19	51.4	7	US-11-202-009-3915	Sequence 3915, Ap
34	19	51.4	7	US-11-202-009-3916	Sequence 3916, Ap
35	19	51.4	7	US-11-202-009-3932	Sequence 3932, Ap
36	19	51.4	7	US-11-202-009-3941	Sequence 3941, Ap
37	19	51.4	9	US-10-073-301A-7	Sequence 7, Appl
38	19	51.4	9	US-10-989-767A-39	Sequence 39, Appl
39	19	51.4	6	US-10-927-435-62	Sequence 62, Appl
40	19	51.4	9	US-10-927-634-62	Sequence 62, Appl
41	19	51.4	9	US-11-203-137-7	Sequence 7, Appl
42	19	51.4	12	US-11-207-078-1739	Sequence 1739, Ap
43	19	51.4	13	US-11-207-078-77	Sequence 77, Appl
44	19	51.4	13	US-11-207-078-93	Sequence 93, Appl
45	19	51.4	15	US-10-522-297-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-11-010-748A-11
Sequence 11, Application US/11010748A
Publication No. US20050244421A1
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMAYER, Wolfgang
APPLICANT: MOELL, Heidrun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
FILE REFERENCE: MER-136
CURRENT APPLICATION NUMBER: US/11/010,748A
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/EP03/06251
PRIOR FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: EP02013423.5
PRIOR FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 926
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(9)
OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
US-11-010-748A-11
Query Match 97.3%; Score 36; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Cy 1 VLXDDLLEA 9
Db 1 VLXDDLLEA 9
RESULT 2
US-11-010-748A-12
Sequence 12, Application US/11010748A
Publication No. US20050244421A1
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMAYER, Wolfgang
APPLICANT: MOELL, Heidrun
APPLICANT: SCHARM, Burkhard

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
; OTHER INFORMATION: all epitopes
US-11-010-748A-12

Query Match          97.3%; Score 36; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VLXDDLLEA 9
Db      1 VLRDDLLER 9

RESULT 3
US-11-172-740-1404
; Sequence 1404, Application US/11172740
; Publication No. US20060057724A1
; GENERAL INFORMATION:
; APPLICANT: MASCIA, Peter
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
; TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
; FILE REFERENCE: 2750-1602PUS2
; CURRENT APPLICATION NUMBER: US/11/172,740
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,621
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/584,829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/584,800
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 2523
; SEQ ID NO 1404
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (208)..(258)
; OTHER INFORMATION: Pfam Name: PHD; Pfam Description: PHD-finger
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for increasing chlorophyll and photosynthetic cap
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making larger plants
; NAME/KEY: misc_feature
; LOCATION:

```

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; OTHER INFORMATION: Utility: Useful for making ornamental plants with modified flower
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confinen
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making taller plants and plants with longer
; OTHER INFORMATION: Inflorescences
US-11-172-740-1404

Query Match          59.5%; Score 22; DB 7; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 VLXDDLLE 8
Db      8 VYVDVYLE 15

RESULT 4
US-10-927-435-63
; Sequence 63, Application US/10927435
; Publication No. US20060045884A1
; GENERAL INFORMATION:
; APPLICANT: MOLDREEM, JEFFREY
; TITLE OF INVENTION: VACCINES FOR AUTOIMMUNE AND INFECTIOUS DISEASE
; FILE REFERENCE: UTSC:78BUC2
; CURRENT APPLICATION NUMBER: US/10/927,435
; CURRENT FILING DATE: 2004-08-26
; PRIOR APPLICATION NUMBER: 60/489,238
; PRIOR FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-927-435-63

Query Match          56.8%; Score 21; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 VLXDDLLE 8
Db      1 ILDDWLE 8

RESULT 5
US-10-927-634-63
; Sequence 63, Application US/10927634
; Publication No. US20060045881A1
; GENERAL INFORMATION:
; APPLICANT: MOLDREEM, JEFFREY
; TITLE OF INVENTION: ANTI-CANCER VACCINES
; FILE REFERENCE: UTSC:78BUC1
; CURRENT APPLICATION NUMBER: US/10/927,634
; CURRENT FILING DATE: 2004-08-26
; PRIOR APPLICATION NUMBER: 60/489,238
; PRIOR FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

```

OTHER INFORMATION: Peptide
US-10-927-634-63

Query Match 56.8%; Score 21; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLXDLLE 8
: |||
Db 1 ILDDWLE 8

RESULT 6
US-10-353-783-71

Sequence 71, Application US/10353783
Publication No. US20050261175A1

GENERAL INFORMATION:

APPLICANT: Zeebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.

Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago
STATE: Illinois

COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/353,783
FILING DATE: 28-Jan-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/448,729

FILING DATE: 24-MAY-1995

APPLICATION NUMBER: 08/172,329

FILING DATE: 21-DEC-1993

APPLICATION NUMBER: 07/982,255

FILING DATE: 25-NOV-1992

APPLICATION NUMBER: 07/684,535

FILING DATE: 10-APR-1991

APPLICATION NUMBER: 07/589,701

FILING DATE: 01-OCT-1990

APPLICATION NUMBER: 07/573,616

FILING DATE: 24-AUG-1990

APPLICATION NUMBER: 07/537,198

FILING DATE: 11-JUN-1990

APPLICATION NUMBER: 07/422,383

FILING DATE: 16-OCT-1989

ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32958A

TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-353-783-71

Query Match 56.8%; Score 21; DB 6; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LXDLLLA 9
: |||
Db 1 IVDLLVA 8

RESULT 7
US-11-129-143-168

Sequence 168, Application US/11129143
Publication No. US20050266518A1

GENERAL INFORMATION:

APPLICANT: BERRY, Alan

APPLICANT: BRETZEL, Werner

APPLICANT: HUMBELIN, Markus

APPLICANT: LOPEZ-ULIBARRI, Rual

APPLICANT: MAYER, Anne F.

APPLICANT: YELISEV, Alexei A.

TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION

FILE REFERENCE: C38435/121966

CURRENT APPLICATION NUMBER: US/11/129,143

CURRENT FILING DATE: 2005-05-13

NUMBER OF SEQ ID NOS: 197

SOFTWARE: PatentIn version 3.1

SEQ ID NO 168

LENGTH: 5

TYPE: PRT

ORGANISM: Bradyrhizobium japonicum

US-11-129-143-168

Query Match 54.1%; Score 20; DB 7; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8
: |||
Db 1 DDLD 5

RESULT 8

US-11-129-143-169

Sequence 169, Application US/11129143
Publication No. US20050266518A1

GENERAL INFORMATION:

APPLICANT: BERRY, Alan

APPLICANT: HUMBELIN, Markus

APPLICANT: LOPEZ-ULIBARRI, Rual

APPLICANT: MAYER, Anne F.

APPLICANT: YELISEV, Alexei A.

TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION

FILE REFERENCE: C38435/121966

CURRENT APPLICATION NUMBER: US/11/129,143

CURRENT FILING DATE: 2005-05-13

NUMBER OF SEQ ID NOS: 197

SOFTWARE: PatentIn version 3.1

SEQ ID NO 169

LENGTH: 5

TYPE: PRT

ORGANISM: Rhizobium sp. strain NGR234

US-11-129-143-169

Query Match 54.1%; Score 20; DB 7; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8
: |||
Db 1 DDLD 5

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RESULT 9
US-11-129-143-170
; Sequence 170, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-11-129-143-170

Query Match          54.1%; Score 20; DB 7; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      4 DDLLE 8
        |||:|:
Db      1 DDILD 5

RESULT 10
US-11-129-143-171
; Sequence 171, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 171
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-11-129-143-171

Query Match          54.1%; Score 20; DB 7; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      4 DDLLE 8
        |||:|:
Db      1 DDILD 5

RESULT 11
US-11-129-143-172
; Sequence 172, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
US-11-129-143-172
```

```
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-129-143-172

Query Match          54.1%; Score 20; DB 7; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      4 DDLLE 8
        |||:|:
Db      1 DDILD 5

RESULT 12
US-11-129-143-173
; Sequence 173, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 173
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-11-129-143-173

Query Match          54.1%; Score 20; DB 7; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      4 DDLLE 8
        |||:|:
Db      1 DDILD 5

RESULT 13
US-10-982-440-126
; Sequence 126, Application US/10982440
; Publication No. US20060018909A1
; GENERAL INFORMATION:
; APPLICANT: Oliner, John
; APPLICANT: Graham, Kevin
; TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
; FILE REFERENCE: 04-881-A
; CURRENT APPLICATION NUMBER: US/10/982,440
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/620,161
; PRIOR FILING DATE: 2004-10-19
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 126
; LENGTH: 7
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-982-440-126

Query Match 54.1%; Score 20; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 7
|||
Db 2 DDL 5

RESULT 14
US-11-021-305-62
Sequence 62, Application US/11021305
Publication No. US20050282733A1
GENERAL INFORMATION:
APPLICANT: Prins, Johannes B
APPLICANT: Hutley, Louise J
TITLE OF INVENTION: Differentiation-modulating agents and uses therefor
FILE REFERENCE: DAV1169.001CPI
CURRENT APPLICATION NUMBER: US/11/021,305
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: USSN 60/392,130
PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.3
SEQ ID NO 62
LENGTH: 8
TYPE: PRT
ORGANISM: mammalian
US-11-021-305-62

Query Match 54.1%; Score 20; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 7
|||
Db 4 DDL 7

RESULT 15
US-11-021-305-65
Sequence 65, Application US/11021305
Publication No. US20050282733A1
GENERAL INFORMATION:
APPLICANT: Prins, Johannes B
APPLICANT: Hutley, Louise J
TITLE OF INVENTION: Differentiation-modulating agents and uses therefor
FILE REFERENCE: DAV1169.001CPI
CURRENT APPLICATION NUMBER: US/11/021,305
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: USSN 60/392,130
PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.3
SEQ ID NO 65
LENGTH: 8
TYPE: PRT
ORGANISM: mammalian
US-11-021-305-65

Query Match 54.1%; Score 20; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 7
|||
Db 4 DDL 7

Search completed: April 6, 2006, 17:29:29
Job time : 13.6667 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:50:52 ; Search time 114 Seconds
(without alignments)
34.688 Million cell updates/sec

Title: US-10-791-217a-2

Perfect score: 45

Sequence: 1 VLHDLLEA 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 770462

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21.*
1: geneeqp1980a:*
2: geneeqp1990a:*
3: geneeqp2000a:*
4: geneeqp2001a:*
5: geneeqp2002a:*
6: geneeqp2003a:*
7: geneeqp2003ba:*
8: geneeqp2004a:*
9: geneeqp2005a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	2	AAW99196
2	45	100.0	9	2	AAW97375
3	45	100.0	9	8	ADH40333
4	45	100.0	13	2	AAW99199
5	45	100.0	13	2	AAW97415
6	37	82.2	9	2	AAW99197
7	37	82.2	9	2	AAW97374
8	37	82.2	9	8	ADH40334
9	37	82.2	13	2	AAW99198
10	37	82.2	13	2	AAW97414
11	36	80.0	9	2	AAW99195
12	36	80.0	9	2	AAW97572
13	31	68.9	9	8	ADU99853
14	30	66.7	9	2	AAW97373
15	29	64.4	13	4	AAU02706
16	28	62.2	9	2	AAV10122
17	28	62.2	9	5	ABG79805
18	28	62.2	9	8	ADK68732
19	28	62.2	9	8	ADK05291
20	28	62.2	9	8	ADK05293
21	28	62.2	9	8	ADQ10530
22	28	62.2	9	8	ADK05295
23	28	62.2	10	8	ADK05295
24	28	62.2	10	8	ADP26019

25	28	62.2	11	7	ADD23269	ADD23269 Breast ca
26	27	60.0	9	6	ABJ20115	ABJ20115 MHC bindi
27	27	60.0	9	8	ADP02787	ADP02787 Human tum
28	27	60.0	10	8	ADQ26722	ADQ26722 Topo V Hn
29	27	60.0	13	4	AAH85071	AAH85071 Human ser
30	27	60.0	13	4	AAH85066	AAH85066 Human ser
31	26	57.8	6	6	ABU97233	ABU97233 Enzyme pe
32	26	57.8	6	6	ABU97232	ABU97232 Enzyme pe
33	26	57.8	6	6	ABU97234	ABU97234 Enzyme pe
34	26	57.8	6	6	ABU97231	ABU97231 Enzyme pe
35	26	57.8	6	6	ADY63770	ADY63770 Human alb
36	26	57.8	7	8	ADM96262	ADM96262 Human ser
37	26	57.8	9	5	AAE31275	AAE31275 Human mag
38	26	57.8	9	8	ADM96261	ADM96261 Human ser
39	26	57.8	9	8	ADM96258	ADM96258 Human ser
40	26	57.8	9	8	ADT73023	ADT73023 Human RSV
41	26	57.8	9	8	ADT49074	ADT49074 Human BFA
42	26	57.8	9	8	ADU99636	ADU99636 BFA5 tumo
43	26	57.8	10	2	AAW73901	AAW73901 B. forsyth
44	26	57.8	10	6	ABP71119	ABP71119 B10 prote
45	26	57.8	10	7	ADM30865	ADM30865 HLA bindi

ALIGNMENTS

RESULT 1
AAW99196
ID AAW99196 standard; peptide; 9 AA.
AAW99196;
20-MAY-1999 (first entry)
Minor histocompatibility antigen HA-1 T-cell epitope #2.
Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
graft versus host disease; bone marrow transplant; leukaemia; vaccine;
diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS Homo sapiens.
XX
PN WO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
(UYLE-) RIUKSUNIV LETDEN.
XX
PI Goulimy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-153312/13.
XX
PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
XX
PT diseases and prevent rejection and host versus graft disease in bone
XX
PS marrow and organ transplantation.
XX
PS Claim 3; Page 32; 47pp; English.
XX
CC The present sequence represents a new peptide (PI) constituting a T-cell
XX
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
XX
CC peptide is immunogenic and can be used as part of a vaccine. PI is used
XX
CC as a medicine, to induce tolerance for transplants, prevent rejection
XX
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
XX
CC particular it can be used with bone marrow transplantation, in the
XX
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
XX
CC diseases
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 45; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
 DB 1 VLHDDLLEA 9

RESULT 2
 AAW97375
 ID AAW97375 standard; protein; 9 AA.
 XX
 AC AAW97375;
 XX
 DT 13-MAY-1999 (first entry)
 XX
 DE HA-1 H-allele sequence.
 XX
 KW Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
 KW R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
 KW severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9905313-A2.
 XX
 PD 04-FEB-1999.
 XX
 PF 23-JUL-1998; 98WO-EP004928.
 XX
 PR 23-JUL-1997; 97EP-00202303.
 XX
 PR 02-JUN-1998; 98EP-00870125.
 XX
 PA (UYLE-) RIJKSUNIV LEIDEN.
 XX
 PI Goujmy E;
 XX
 DR WPI; 1999-142960/12.
 XX
 PT Typing minor histocompatibility antigen HA-1 - by amplifying and
 PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
 PT of genetic aberrances.
 XX
 PS Claim 18; Fig 5; 59pp; English.
 XX
 CC The present sequence represents part of the minor histocompatibility
 CC antigen HA-1-H-allele. The specification describes methods for typing
 CC alleles (preferably the H and R alleles) of the minor histocompatibility
 CC antigen HA-1 in a sample, which comprise detecting polymorphic
 CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
 CC methods can be used for HA-1 typing for bone marrow transplants, severe
 CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
 CC detection of genetic aberrances. The probes and primers of the invention
 CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
 CC anti-idiotypic B cells and/or T cells and antibodies
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 45; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
 DB 1 VLHDDLLEA 9

RESULT 3
 ADH40333
 ID ADH40333 standard; peptide; 9 AA.
 XX
 AC ADH40333;

XX 11-MAR-2004 (first entry)
 DT
 XX
 DE Human minor histocompatibility antigen HA-1 T cell epitope.
 KW human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
 KW minor histocompatibility antigen; mAb; T cell epitope.
 XX
 OS Homo sapiens.
 XX
 PN WO2003106692-A2.
 XX
 PD 24-DEC-2003.
 XX
 PF 13-JUN-2003; 2003WO-BP006251.
 XX
 PR 13-JUN-2002; 2002EP-00013423.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Strittmatter W, Moll H;
 XX
 DR WPI; 2004-082200/08.
 XX
 PT Providing allelic variant epitope of protein based on single nucleotide
 PT polymorphism by defining target protein, screening database of protein,
 PT identifying, selecting allelic variant protein, creating variant
 PT epitopes.
 XX
 PS Disclosure; Page 82; 119pp; English.

XX The invention relates to a novel method for providing epitopes of allelic
 CC variants of antigenic proteins from specific species based on single
 CC nucleotide polymorphism (SNP), by defining target protein/peptide or its
 CC subset, screening database of DNA encoding target protein, identifying,
 CC selecting allelic peptide/protein variants, expression product or its
 CC fragment encoded by DNA sequence having SNP, creating variant epitopes,
 CC selecting epitopes binding to MHC protein. A protein of the invention has
 CC cytostatic activity, and may have a use in a vaccine. The method is
 CC useful for generating a SNP profile of one or more individuals from a
 CC given species by applying the method for several protein from the
 CC individuals, where the SNP profile was related to disease, preferably
 CC cancer. This is useful for diagnosing a disease in an individual by
 CC generating the SNP-related polymorphic profile. A method of the invention
 CC is useful for transplanting haematopoietic stem cells from a donor to a
 CC recipient and treating cancer, preferably leukaemia, and for determining
 CC the progression, regression or onset of a treated disease. The present
 CC sequence is used in the exemplification of the invention.

XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 45; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
 DB 1 VLHDDLLEA 9

RESULT 4
 AAW99199
 ID AAW99199 standard; peptide; 13 AA.
 XX
 AC AAW99199;
 XX
 DT 20-MAY-1999 (first entry)
 XX
 DE VR cell KIAA0223 protein sequence.
 XX
 KW Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
 KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
 KW diagnosis; aplastic anaemia; immune deficiency disease.

XX Synthetic.
 OS WO9905174-A1.
 XX PD 04-FEB-1999.
 XX PF 23-JUL-1998; 98WO-NL000425.
 XX PR 23-JUL-1997; 97EP-00202303.
 XX (UYLE-) RIKKSUNIV LEIDEN.
 XX PA Goulmy EAJM, Hunt DF, Engelhard VH;
 XX DR WPI; 1999-153312/13.
 XX DR N-PSDB; AAX19409.
 XX PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
 XX PT diseases and prevent rejection and host versus graft disease in bone
 XX PT marrow and organ transplantation.
 XX PS Disclosure; Page 31; 47pp; English.
 XX CC The present invention describes a new peptide (P1) constituting a T-cell
 XX CC epitope obtainable from the minor histocompatibility antigen HA-1. The
 XX CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
 XX CC as a medicine, to induce tolerance for transplants, prevent rejection
 XX CC and/or graft versus host disease, or to treat (auto) immune diseases. In
 XX CC particular it can be used with bone marrow transplantation, in the
 XX CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
 XX CC diseases. The present sequence represents a KIAA0223 sequence given in
 XX CC the present invention
 XX SQ Sequence 13 AA;
 XX
 XX Query Match 100.0%; Score 45; DB 2; Length 13;
 XX Best Local Similarity 100.0%; Pred. No. 0.17;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VHDDLLEA 9
 Db 3 VHDDLLEA 11
 DB
 RESULT 5
 AAW97415
 ID AAW97415 standard; protein; 13 AA.
 XX AC AAW97415;
 XX DT 20-MAY-1999 (first entry)
 XX DE KIAA0223 polymorphism in HA-1 positive homozygous individuals.
 XX XX
 XX T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
 XX KW transplant rejection; Graft-versus-host disease; autoimmune disease;
 XX KW neoplastic haematopoietic cell; KIAA0223 polymorphism.
 XX XX
 XX OS Homo sapiens.
 XX XX WO9905173-A1.
 XX PM 04-FEB-1999.
 XX PD 23-JUL-1998; 98WO-NL000424.
 XX PF 23-JUL-1997; 97EP-00202303.
 XX PR (UYLE-) RIKKSUNIV LEIDEN.
 XX PA Goulmy EAJM, Hunt DF, Engelhard VH;
 XX PI
 XX CC

DR WPI; 1999-142855/12.
 DR N-PSDB; AAX16081.
 XX PT Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
 XX PT for inducing tolerance to transplants and prevent rejection or graft-
 XX PT versus-host disease.
 XX PS Disclosure; Page 38; 57pp; English.
 XX XX
 XX CC The present sequence represents the KIAA0223 polymorphism in HA-1
 XX CC positive homozygous individuals. The specification describes an
 XX CC immunogenic peptide constituting a T-cell epitope, obtainable from the
 XX CC minor histocompatibility antigen HA-1. The peptide can be used in
 XX CC vaccines or pharmaceutical formulations as medicines to induce tolerance
 XX CC for transplants so as to prevent rejection and/or Graft-versus-host
 XX CC disease, or to treat autoimmune diseases. Neoplastic haematopoietic cells
 XX CC presenting the peptides, in an HLA class I context, can be eliminated
 XX CC after specific recognition of the peptides. The peptides can also be used
 XX CC to raise antibodies, T-cell receptor, B- and T-cells
 XX SQ Sequence 13 AA;
 XX
 XX Query Match 100.0%; Score 45; DB 2; Length 13;
 XX Best Local Similarity 100.0%; Pred. No. 0.17;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VHDDLLEA 9
 Db 3 VHDDLLEA 11
 DB
 RESULT 6
 AAW99197
 ID AAW99197 standard; peptide; 9 AA.
 XX AC AAW99197;
 XX DT 20-MAY-1999 (first entry)
 XX DE Minor histocompatibility antigen HA-1 T-cell epitope #3.
 XX XX
 XX Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
 XX KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
 XX KW diagnosis; aplastic anaemia; immune deficiency disease.
 XX XX
 XX OS Homo sapiens.
 XX XX WO9905174-A1.
 XX PN 04-FEB-1999.
 XX PD 23-JUL-1998; 98WO-NL000425.
 XX PF 23-JUL-1997; 97EP-00202303.
 XX PR (UYLE-) RIKKSUNIV LEIDEN.
 XX PA Goulmy EAJM, Hunt DF, Engelhard VH;
 XX PI
 XX DR WPI; 1999-153312/13.
 XX PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
 XX PT diseases and prevent rejection and host versus graft disease in bone
 XX PT marrow and organ transplantation.
 XX PS Disclosure; Page 15; 47pp; English.
 XX CC The present sequence represents a new peptide (P1) constituting a T-cell
 XX CC epitope obtainable from the minor histocompatibility antigen HA-1. The
 XX CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
 XX CC as a medicine, to induce tolerance for transplants, prevent rejection
 XX CC and/or graft versus host disease, or to treat (auto) immune diseases. In
 XX CC particular it can be used with bone marrow transplantation, in the

CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
 CC diseases
 XX
 SQ Sequence 9 AA;

Query Match 82.2%; Score 37; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLHDDLLEA 9
 |||||
 1 VLHDDLLEA 9

RESULT 7
 AAM97374
 ID AAM97374 standard; protein; 9 AA.

XX AAM97374;

DT 13-MAY-1999 (first entry)

XX HA-1 R-allele sequence.

XX Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
 KW R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
 KW severe aplastic anaemia; leukaemia; immune deficiency disease; ss.

XX Homo sapiens.

XX WO9905313-A2.

XX 04-FEB-1999.

XX 23-JUL-1998; 98WO-EP004928.

XX 23-JUL-1997; 97EP-00202303.

XX 02-JUN-1998; 98BP-00870125.

XX (UYLE-) RIKSUNIV LEIDEN.

XX Goulmy E;

XX WPI; 1999-142960/12.

PT Typing minor histocompatibility antigen HA-1 - by amplifying and
 PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
 PT of genetic aberrances.

XX Claim 13; Fig 5; 59pp; English.

XX The present sequence represents part of the minor histocompatibility
 CC antigen HA-1 R-allele. The specification describes methods for typing
 CC alleles (preferably the H and R alleles) of the minor histocompatibility
 CC antigen HA-1 in a sample, which comprise detecting polymorphic
 CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
 CC methods can be used for HA-1 typing for bone marrow transplants, severe
 CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
 CC detection of genetic aberrances. The probes and primers of the invention
 CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
 CC anti-idiotypic B cells and/or T cells and antibodies
 XX
 SQ Sequence 9 AA;

Query Match 82.2%; Score 37; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLHDDLLEA 9
 |||||
 1 VLHDDLLEA 9

RESULT 8
 ADH40334
 ID ADH40334 standard; peptide; 9 AA.

XX ADH40334;

DT 11-MAR-2004 (first entry)

XX Human minor histocompatibility antigen HA-1 T cell epitope.

XX human; cytostatic; vaccine; SNP profile; cancer; leukaemia;

KW minor histocompatibility antigen; mHAg; T cell epitope.

XX Homo sapiens.

XX WO2003106692-A2.

XX 24-DEC-2003.

XX 13-JUN-2003; 2003WO-EP006251.

XX 13-JUN-2002; 2002BP-00013423.

XX (MERE) MERCK PATENT GMBH.

XX Stittmatter W, Moll H;

XX WPI; 2004-082200/08.

PT Providing allelic variant epitope of protein based on single nucleotide
 PT polymorphism by defining target protein, screening database of protein,
 PT identifying, selecting allelic variant protein, creating variant
 PT epitopes.

XX Disclosure; Page 82; 119pp; English.

XX The invention relates to a novel method for providing epitopes of allelic
 CC variants of antigenic proteins from specific species based on single
 CC nucleotide polymorphism (SNP), by defining target protein/peptide or its
 CC subset, screening database of DNA encoding target protein, identifying,
 CC selecting allelic peptide/protein variants, expression product or its
 CC fragment encoded by DNA sequence having SNP, creating variant epitopes,
 CC selecting epitopes binding to MHC protein. A protein of the invention has
 CC cytostatic activity, and may have a use in a vaccine. The method is
 CC useful for generating a SNP profile of one or more individuals from a
 CC given species by applying the method for several protein from the
 CC individuals, where the SNP profile was related to disease, preferably
 CC cancer. This is useful for diagnosing a disease in an individual by
 CC generating the SNP-related polymorphic profile. A method of the invention
 CC is useful for transplanting haematopoietic stem cells from a donor to a
 CC recipient and treating cancer, preferably leukaemia, and for determining
 CC the progression, regression or onset of a treated disease. The present
 CC sequence is used in the exemplification of the invention.

XX Sequence 9 AA;

Query Match 82.2%; Score 37; DB 8; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLHDDLLEA 9
 |||||
 1 VLHDDLLEA 9

RESULT 9
 AAM99198
 ID AAM99198 standard; peptide; 13 AA.

XX AAM99198;

DT 20-MAY-1999 (first entry)

DE	DH	cellK1AA0223	protein sequence.
XX			
KM	Minor	histocompatibility antigen; HA-1; T-cell epitope; immunological;	
KW	graft	versus host disease; bone marrow transplant; leukaemia; vaccine;	
KW	diagnosis;	aplastic anaemia; immune deficiency disease.	
XX			
OS	Synthetic.		
XX			
PN	W09905174-A1.		
XX			
PD	04-FEB-1999.		
XX			
PF	23-JUL-1998;	98WO-NL000425.	
XX			
PR	23-JUL-1997;	97EP-00202303.	
XX			
PA	(UYLE-) RIJXSUNIV LEIDEN.		
XX			
PI	Goulimy EAJM, Hunt DF, Engelhard VH;		
XX			
DR	WPI; 1999-153312/13.		
DR	N-PSDB; AAX19408.		
XX			
PT	A new minor histocompatibility antigen, HA-1 - useful to treat immune		
PT	diseases and prevent rejection and host versus graft disease in bone		
PT	marrow and organ transplantation.		
XX			
PS	Disclosure; Page 31; 47pp; English.		
XX			
CC	The present invention describes a new peptide (PI) constituting a T-cell		
CC	epitope obtainable from the minor histocompatibility antigen HA-1. The		
CC	peptide is immunogenic and can be used as part of a vaccine. PI is used		
CC	as a medicine, to induce tolerance for transplants, prevent rejection		
CC	and/or graft versus host disease, or to treat (auto) immune diseases. In		
CC	particular it can be used with bone marrow transplantation, in the		
CC	treatment of severe aplastic anaemia, leukaemia, and immune deficiency		
CC	diseases. The present sequence represents a K1AA0223 sequence given in		
CC	the present invention		
XX			
SQ	Sequence 13 AA;		
	Query Match	82.2%;	Score 37; DB 2; Length 13;
	Best Local Similarity	88.9%;	Pred. No. 5.1;
	Matches 8; Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
Oy	1 VLHDDLEA 9		
Db	3 VLRDDLEA 11		
RESULT 10			
ID	AAW97414		
XX	AAW97414 standard; protein; 13 AA.		
AC			
XX	AAW97414;		
XX			
DT	20-MAY-1999 (first entry)		
XX			
DE	K1AA0223 polymorphism in HA-1 negative homozygous individuals.		
XX			
KW	T-cell epitope; minor histocompatibility antigen HA-1; vaccine;		
KW	transplant rejection; Graft-versus-Host Disease; autoimmune disease;		
KW	neoplastic haematopoietic cell; K1AA0223 polymorphism.		
XX			
OS	Homo sapiens.		
XX			
PN	W09905173-A1.		
XX			
PD	04-FEB-1999.		
XX			
PF	23-JUL-1998;	98WO-NL000424.	
XX			
PR	23-JUL-1997;	97EP-00202303.	
XX			

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XX (UTLE-) RIJXSUNIV LEIDEN.
PA
PI Goulmv EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-142855/12.
XX
DR N-PSDB; AAXI6080.
XX
XX Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
PT for inducing tolerance to transplants and prevent rejection or graft-
PT versus-host disease.
XX
XX Disclosure; Page 38; 57pp; English.
XX
XX The present sequence represents the KIAA0223 polymorphism in HA-1
CC negative homozygous individuals. The specification describes an
CC immunogenic peptide constituting a T-cell epitope, obtainable from the
CC minor histocompatibility antigen HA-1. The peptide can be used in
CC vaccines or pharmaceutical formulations as medicines to induce tolerance
CC for transplants so as to prevent rejection and/or graft-versus-host
CC disease, or to treat autoimmune diseases. Neoplastic haematopoietic cells
CC presenting the peptides, in an HLA class I context, can be eliminated
CC after specific recognition of the peptides. The peptides can also be used
CC to raise antibodies, T-cell receptor, B- and T-cells
XX
XX Sequence 13 AA;
SQ
Query Match 82.2%; Score 37; DB 2; Length 13;
Best Local Similarity 88.9%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 VHHDDLLEA 9
||| |||||
DB 3 VLRDDLLEA 11
||| |||||
RESULT 11
AAW99195
AAW99195 standard; peptide; 9 AA.
XX
AC AAW99195;
XX
DT 20-MAY-1999 (first entry)
XX
DE Minor histocompatibility antigen HA-1 T-cell epitope #1.
XX
KW Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW graft versus host disease; bone marrow transplant; leukemia; vaccine;
KW diagnosis; aplastic anaemia; immune deficiency disease.
XX
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 3
FT /label= His, Arg
XX
PM W09905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
XX (UTLE-) RIJXSUNIV LEIDEN.
PA
XX Goulmv EAJM, Hunt DF, Engelhard VH;
XX
XX WPI; 1999-153312/13.
XX
XX A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone

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PT marrow and organ transplantation.
XX
XX Claim 1; Page 32; 47pp; English.
XX
CC The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases
XX
SQ Sequence 9 AA;

Query Match      80.0%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
   |||||
Db 1 VLXDDLLEA 9

RESULT 12
AAW97572
ID AAW97572 standard; peptide; 9 AA.
AC AAW97572;
XX
XX 20-MAY-1999 (first entry)
XX
DE T-cell epitope from the minor histocompatibility antigen HA-1.
XX
XX T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
XX transplant rejection; Graft-versus-Host Disease; autoimmune disease;
XX neoplastic haematopoietic cell.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 3 /note= "His or Arg"
XX
XX WO905173-A1.
XX
XX 04-FEB-1999.
XX
XX 23-JUL-1998; 98WO-NL000424.
XX
XX 23-JUL-1997; 97EP-00202303.
XX
XX (UYLE-) RIKKSUNIV LEIDEN.
XX
XX Goulmy EAJM, Hunt DF, Engelhard VH;
XX WPI; 1999-142855/12.
XX
XX Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
XX for inducing tolerance to transplants and prevent rejection or graft-
XX versus-host disease.
XX
XX Claim 1; Page 39; 57pp; English.
XX
XX The present sequence represents an immunogenic peptide constituting a T-
XX cell epitope, obtainable from the minor histocompatibility antigen HA-1.
XX The peptide can be used in vaccines or pharmaceutical formulations as
XX medicines to induce tolerance for transplants so as to prevent rejection
XX and/or Graft-versus-Host Disease, or to treat autoimmune diseases.
XX Neoplastic haematopoietic cells presenting the peptides, in an HLA class
XX I context, can be eliminated after specific recognition of the peptides.
XX The peptides can also be used to raise antibodies, T-cell receptor, B-
XX and T-cells

```

```

XX
SQ Sequence 9 AA;

Query Match      80.0%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
   |||||
Db 1 VLXDDLLEA 9

RESULT 13
ADU99853
ID ADU99853 standard; peptide; 9 AA.
AC ADU99853;
XX
XX 24-FEB-2005 (first entry)
XX
DE BC24 tumor antigen antigenic peptide #85.
XX
XX expression vector; tumor antigen; cancer; cytostatic; BC24;
XX antigenic peptide.
XX
XX Unidentified.
XX
XX WO2004104039-A2.
XX
XX 02-DEC-2004.
XX
XX 15-MAY-2004; 2004WO-US015202.
XX
XX 16-MAY-2003; 2003US-0471139P.
XX
XX 16-MAY-2003; 2003US-0471139P.
XX
XX (AVENT ) AVENTIS PASTEUR INC.
XX
XX Berinstein N, Gallichan S, Lovitt C, Farrington M, Radvanyi L;
XX Singh-Sandhu D;
XX WPI; 2004-834272/82.
XX
XX New expression vector comprising a nucleic acid encoding a tumor antigen,
XX e.g. BFA4, BCY1, BFA5, BC24, or BFY3, useful for expressing multiple
XX tumor antigens, or for preventing or treating cancer.
XX
XX Example 8; Page 60; 109pp; English.
XX
XX The invention comprises an expression vector that contains a nucleic acid
XX encoding a tumor antigen (e.g. BC24 or BFY3). The expression vector of
XX the invention is useful for the expression of multiple tumor antigens and
XX the prevention or treatment of cancer. The present amino acid sequence
XX represents a BC24 tumor antigen antigenic peptide that was used in an
XX example of the invention.
XX
XX Sequence 9 AA;

Query Match      68.9%; Score 31; DB 8; Length 9;
Best Local Similarity 85.7%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LHSDDLLE 8
   |||||
Db 2 LHSDDLLE 8

RESULT 14
AAW97373
ID AAW97373 standard; peptide; 9 AA.
AC AAW97373;
XX

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DT 13-MAY-1999 (first entry)
 XX Peptide epitope of HA-1 antigen.
 DE
 XX
 XX Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
 KM R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
 KM severe aplastic anaemia; leukaemia; immune deficiency disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 2 /note= "not specified"
 FT Misc-difference 6 /note= "not specified"
 FT Misc-difference 7 /note= "not specified"
 FT Misc-difference 7 /note= "not specified"
 XX
 PN WO9905313-A2.
 XX
 XX 04-FEB-1999.
 PD
 XX
 PF 23-JUL-1998; 98WO-BP004928.
 XX
 PR 23-JUL-1997; 97EP-00202303.
 PR 02-JUN-1998; 98EP-00870125.
 XX
 PA (UYLE-) RIUKSUNIV LEIDEN.
 XX
 PI Goulmy E;
 XX
 DR WPI; 1999-142960/12.
 XX
 PT Typing minor histocompatibility antigen HA-1 - by amplifying and
 PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
 PT of genetic aberrances.
 XX
 PS Example 1; Page 22; 59pp; English.
 XX
 XX The present sequence represents an epitope of the minor
 CC histocompatibility antigen HA-1. The specification describes methods for
 CC typing alleles (preferably the H and R alleles) of the minor
 CC histocompatibility antigen HA-1 in a sample, which comprise detecting
 CC polymorphic nucleotides in the cDNA or genomic nucleic acids of the
 CC alleles. The methods can be used for HA-1 typing for bone marrow
 CC transplants, severe aplastic anaemia, leukaemia and immune deficiency
 CC diseases, as well as detection of genetic aberrances. The probes and
 CC primers of the invention can be used to screen for the HA-1 alleles. The
 CC HA-1 peptides can be used anti-idiotypic B cells and/or T cells and
 CC antibodies
 CC
 SO Sequence 9 AA;
 Query Match 66.7%; Score 30; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2e+06; 3; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 VLHDDLRA 9
 | | | | |
 Db 1 VXHDXXA 9
 | | | | |
 RESULT 15
 AAU02706
 ID AAU02706 standard; peptide; 13 AA.
 XX
 AC AAU02706;
 XX
 XX 29-AUG-2001 (first entry)
 DT
 XX CDR region of anti-adipocyte antibody heavy chain, FAT 71.
 DE
 XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;

KM heart disease; complementarity determining region; CDR.
 XX
 XX Homo sapiens.
 OS
 XX WO200127279-A1.
 PN
 XX
 XX 19-APR-2001.
 PD
 XX
 PF 11-OCT-2000; 2000WO-GB003900.
 XX
 XX 12-OCT-1999; 99US-0158812P.
 PR
 XX
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Edwards BM, Main SH, Vaughan TJ;
 XX
 DR WPI; 2001-282031/29.
 DR N-PSDB; AAS03483.
 XX
 PT Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.
 XX
 PS Example 7; Page 78; 182pp; English.
 XX
 CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease
 CC
 SO Sequence 13 AA;
 Query Match 64.4%; Score 29; DB 4; Length 13;
 Best Local Similarity 62.5%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 VLHDDLRA 8
 | | | | |
 Db 5 VVHDDAPE 12
 | | | | |
 Search completed: April 6, 2006, 16:57:03
 Job time : 115 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 6, 2006, 16:57:26 ; Search time 19 seconds
(without alignments)
45.576 Million cell updates/sec

Title: US-10-791-217A-2

Perfect score: 45
Sequence: 1 VLHDDLRA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	46.7	15	2 A53594	calnexin - mouse (
2	19	42.2	15	2 S30608	translation elonga
3	19	42.2	15	2 A45096	thyrotropin-releas
4	18	40.0	7	2 I46868	alpha-myosin heavy
5	18	40.0	10	2 B59272	peptide-N4-(N-acet
6	18	40.0	10	2 C26997	unspecific monooxy
7	18	40.0	15	2 S29485	GRP-binding protei
8	18	40.0	15	2 B56819	PS I complex subun
9	18	40.0	15	2 A26997	unspecific monooxy
10	17	37.8	9	2 S55696	phosphoenolpyruvat
11	17	37.8	10	2 S13224	viro protein - Agr
12	17	37.8	10	2 S30348	clotting protein -
13	17	37.8	11	2 PH0924	T-cell receptor be
14	17	37.8	12	2 S39762	cytochrome P450 UT
15	17	37.8	13	2 PS0443	potassium channel
16	17	37.8	14	2 S50900	chlorophyll a/b-bi
17	17	37.8	14	2 S74128	superoxide dismuta
18	17	37.8	14	2 C39170	acyl-lacyl-carrier
19	17	37.8	15	2 S62675	collagen type I -
20	16	35.6	7	2 PQ0663	membrane protein -
21	16	35.6	7	2 S68004	hucolin, 75K chain
22	16	35.6	8	2 PC4131	hypothetical prote
23	16	35.6	10	1 SPRGNK	neurotrophin X - pig
24	16	35.6	10	2 A61354	carotene medium/l
25	16	35.6	10	2 P44644	neurotoxin-associ
26	16	35.6	11	2 S78765	ribosomal protein
27	16	35.6	13	2 G44644	neurotoxin-associ
28	16	35.6	13	2 S14316	photosystem I 9K c
29	16	35.6	14	1 LFEBWC	trp operon leader

30	16	35.6	14	2 S29789	hypothetical prote
31	16	35.6	14	2 S48685	extension protein
32	16	35.6	15	2 S14749	3-dehydroquinase -
33	16	35.6	15	2 B32800	hypothetical prote
34	16	35.6	15	2 B26501	lipoprotein lipase
35	15	33.3	6	2 S78764	ribosomal protein
36	15	33.3	7	2 A59489	protein kinase C 1
37	15	33.3	11	2 A14454	6-phosphofructokin
38	15	33.3	11	2 S41909	hypothetical prote
39	15	33.3	13	2 PT0256	Ig heavy chain CRD
40	15	33.3	13	2 S65612	tubulin alpha-chain
41	15	33.3	13	2 S00316	photosystem I 13K
42	15	33.3	14	2 PH1626	Ig H chain V-D-J r
43	15	33.3	14	2 A61306	ribonuclease M (EC
44	15	33.3	15	2 PA0009	seed storage prote
45	15	33.3	15	2 PQ0750	self-incompatibili

ALIGNMENTS

RESULT 1
A53594
calnexin - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C:Accession: A53594
R:Jentner, M.; Vestweber, D.
J. Biol. Chem. 269, 12263-12268, 1994
A:Title: The integrin chains beta-1 and alpha-6 associate with the chaperone calnexin pr
A:Reference number: A53594; MUID:94216347; PMID:8163531
A:Accession: A53594
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <LEN>
A:Cross-references: UNIPROT:Q7M063; UNIPARC:UPI000017C62E
C:Keywords: endoplasmic reticulum; molecular chaperone

Query Match
Best Local Similarity 46.7%; Score 21; DB 2; Length 15;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDL 6
DB 10 IIEDDL 15

RESULT 2

S30608
translation elongation factor eEF-2 - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 07-May-1999
C:Accession: S30608
R:Brown, B.A.; Bodley, J.W.
FEBS Lett. 103, 253-255, 1979
A:Title: Primary structure at the site in beef and wheat elongation factor 2 of ADP-ribo
A:Reference number: S30607; MUID:79236796; PMID:467667
A:Molecule type: protein
A:Residues: 1-15 <BRO>
A:Cross-references: UNIPARC:UPI000017482A
C:Keywords: GTP binding; protein biosynthesis

Query Match
Best Local Similarity 42.2%; Score 19; DB 2; Length 15;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LHDDLRA 9
DB 3 VHDVTLRA 10

```
RESULT 3
A:Accession: A45096
A:Title: thyrotropin-releasing hormone receptor, splice form 387 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A45096
R:de la Pena, P.; Delgado, L.M.; del Camino, D.; Barros, F.
J. Biol. Chem. 267, 25703-25708, 1992
A:Title: Two isoforms of the thyrotropin-releasing hormone receptor generated by alterna
A:Reference number: A45096; MUID:93100278; PMID:1334485
A:Accession: A45096
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-15 <DB>
A:Cross-references: UNIPARC:UPI0000170C44; GB:S51512; NID:g261982; PIDN:AA24549.1; PID:
A:Experimental source: GH3 anterior pituitary cells
A>Note: sequence extracted from NCBI backbone (NCBIP:120927)

Query Match
Best Local Similarity 42.2%; Score 19; DB 2; Length 15;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDL 7
Db 9 LVHMDIL 15

RESULT 4
A:Accession: I46868
A:Title: alpha-myosin heavy chain - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C:Accession: I46868
R:Friedman, D.U.; Umeda, P.K.; Sinha, A.M.; Hsu, H.
Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984
A:Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricula
A:Reference number: I46868; MUID:84221901; PMID:6328491
A:Accession: I46868
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7 <FRI>
A:Cross-references: UNIPROT:Q28742; UNIPARC:UPI0000087938; GB:K01698; NID:g165538; PIDN:

Query Match
Best Local Similarity 40.0%; Score 18; DB 2; Length 7;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHDD 5
Db 3 MHDE 6

RESULT 5
A:Accession: B59272
A:Title: peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain -
N:Alternate names: peptide N-glycosidase
C:Species: Prunus dulcis var. sativa (sweet almond)
C>Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: B59272
R:Altman, F.; Paschinger, K.; Dalik, T.; Vorauer, K.
Eur. J. Biochem. 252, 118-123, 1998
A:Title: Characterization of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A
A:Reference number: A59272; MUID:98181894; PMID:9523720
A:Accession: B59272
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <ALT>
A:Cross-references: UNIPROT:P61896; UNIPARC:UPI00000ABBC4
C:Keywords: hydrolase

Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 LHD 4
Db 5 LHD 7

RESULT 6
A:Accession: C26997
A:Title: unspecific monooxygenase (EC 1.14.14.1) isozyme B, phenobarbital-inducible, hepatic - ra
N:Alternate names: cytochrome P450
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-2004
C:Accession: C26997
R:Graves, P.E.; Kaminsky, L.S.; Halpert, J.
Biochemistry 26, 3887-3894, 1987
A:Title: Evidence for functional and structural multiplicity of pregnenolone-16-alpha-ca
A:Reference number: A26997; MUID:88000604; PMID:3651420
A:Accession: C26997
A:Molecule type: protein
A:Residues: 1-10 <GRA>
A:Cross-references: UNIPROT:Q06884; UNIPARC:UPI0000174DA8
A:Superfamily: cytochrome P450 homology
C:Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembrane

Query Match
Best Local Similarity 40.0%; Score 18; DB 2; Length 10;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DLEA 9
Db 2 DLISA 6

RESULT 7
A:Accession: S29485
A:Title: GTP-binding protein o-ral - Pacific electric ray (fragment)
C:Species: Torpedo californica (Pacific electric ray)
C>Date: 22-Nov-1993 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
C:Accession: S29485
R:Volkmann, W.; Pevsner, J.; Elferink, L.A.; Scheller, R.H.
FEBS Lett. 317, 53-56, 1993
A:Title: Association of three small GTP-binding proteins with cholinergic synaptic vesic
A:Reference number: S29485; MUID:93154521; PMID:8428634
A:Accession: S29485
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <VOL>
A:Cross-references: UNIPARC:UPI000017BF33

Query Match
Best Local Similarity 40.0%; Score 18; DB 2; Length 15;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 LHDDLE 8
Db 1 MYDEPVE 7

RESULT 8
A:Accession: E56819
A:Title: PS I complex subunit 8 - cucumber (fragment)
C:Species: Cucumis sativus (cucumber)
C>Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C:Accession: E56819
R:Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.
Biochim. Biophys. Acta 1059, 141-148, 1991
A:Title: Characterization of genes that encode subunits of cucumber PS I complex by N-ter
A:Reference number: A56819; MUID:91355209; PMID:1883835
A:Accession: E56819
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <IWA>
A:Cross-references: UNIPROT:P42052; UNIPARC:UPI0000132593
```

A>Note: sequence extracted from NCBI backbone (NCBIP:58606)

Query Match 40.0%; Score 18; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLHDD 5
|:|
Db 10 VIQDD 14

RESULT 9

A26997

unspecific monoxygenase (EC 1.14.14.1) cytochrome P450 2B1, hepatic - rat (fragment)

N:Alternate names: cytochrome P450b

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-2004

C:Accession: A26997

R:Graves, P.E.; Kaminsky, L.S.; Halpert, J.

Biochemistry 26, 3887-3894, 1987

A:Title: Evidence for functional and structural multiplicity of pregnenolone-16-alpha-c

A:Reference number: A26997; MUID:8800604; PMID:3651420

A:Accession: A26997

A:Molecule type: protein

A:Residues: 1-15 <GRA>

A:Cross-references: UNIPROT:Q06884; UNIPARC:UPI0000174DA7

C:Superfamily: cytochrome P450 homology

C:Keywords: electron transfer; heme; liver; monoxygenase; oxidoreductase; transmembrane

Query Match 40.0%; Score 18; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.6e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 DLHSA 9
|||
Db 2 DLHSA 6

RESULT 10

S55696

phosphoenolpyruvate carboxykinase - Trypanosoma brucei

C:Species: Trypanosoma brucei

C>Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C:Accession: S55696

R:Hunt, M.; Koehler, P.

Biochim. Biophys. Acta 1249, 15-22, 1995

A:Title: Purification and characterization of phosphoenolpyruvate carboxykinase from Try

A:Reference number: S55696; MUID:95284106; PMID:7766679

A:Accession: S55696

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-9 <HUN>

A:Cross-references: UNIPROT:Q7M355; UNIPARC:UPI000017B599

Query Match 37.8%; Score 17; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLHDD 6
||:|
Db 3 IHHKUL 8

RESULT 11

S13224

virg protein - Agrobacterium sp. (fragment)

C:Species: Agrobacterium sp.

C>Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004

C:Accession: S13224

R:Tamamoto, S.; Aoyama, T.; Takanami, M.; Oka, A.

J. Mol. Biol. 215, 537-547, 1990

A:Title: Binding of the regulatory protein VirG to the phased signal sequences upstream

A:Reference number: S13224; MUID:91039316; PMID:2231718

A:Accession: S13224

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <TAM>

A:Cross-references: UNIPROT:Q7MOP7; UNIPARC:UPI000017A9C4

Query Match 37.8%; Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLHDD 5
||:|
Db 6 VIQDD 10

RESULT 12

S30348

clotting protein - signal crayfish

C:Species: Pacifastacus leniusculus (signal crayfish)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C:Accession: S30348

R:Kopacek, P.; Hall, M.; Soederhaell, K.

Eur. J. Biochem. 213, 591-597, 1993

A:Title: Characterization of a clotting protein, isolated from plasma of the freshwater

A:Reference number: S30348; MUID:93238739; PMID:8097463

A:Accession: S30348

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <KOP>

A:Cross-references: UNIPROT:P81070; UNIPROT:Q9UAR3; UNIPARC:UPI000017BDEA

Query Match 37.8%; Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.5e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 LHDDL 6
||:|
Db 1 LHSNL 5

RESULT 13

PH0924

T-cell receptor beta chain V-D-J region (isolate 10) - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C:Accession: PH0924

R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy

A:Reference number: PH0924; MUID:92078857; PMID:1836012

A:Accession: PH0924

A:Molecule type: mRNA

A:Residues: 1-11 <GOL>

A:Cross-references: UNIPARC:UPI000017C9F3

A:Experimental source: concanavalin A-activated lymphoblast

C:Keywords: T-cell receptor

Query Match 37.8%; Score 17; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 DLHSA 8
||:|
Db 7 DLHSA 10

RESULT 14

S39762

cytochrome P450 UT-7b - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995

C:Accession: S39762

R:Ohishi, N.; Imaka, S.; Suzuki, T.; Funae, Y.

Biochim. Biophys. Acta 1158, 227-236, 1993

A;Title: Characterization of two P-450 isozymes placed in the rat CYP2D subfamily.

A;Reference number: S39761; MUID:94072607; PMID:8251521

A;Accession: S39762

A;Molecule type: protein

A;Residues: 1-12 <OH>

A;Cross-references: UNIPARC:UPI000017C8F7

Query Match 37.8%; Score 17; DB 2; Length 12;

Best Local Similarity 50.0%; Pred. No. 3.1e+03;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDL 6

Db 3 LIQDDL 8

RESULT 15

PS0443 potassium channel protein S10 G3 - fruit fly (*Drosophila melanogaster*) (fragment)

C;Species: *Drosophila melanogaster*

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Feb-1997

C;Accession: PS0443

R;Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Bond

Neuron 9, 209-216, 1992

A;Title: Calcium-activated potassium channels expressed from cloned complementary DNAs.

A;Reference number: JH0697; MUID:92360298; PMID:1497890

A;Accession: PS0443

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-13 <ADR>

A;Cross-references: UNIPARC:UPI000017BEBA

C;Comment: This potassium channel is activated by calcium.

C;Genetics:

A;Gene: FlyBase:s10

A;Cross-references: FlyBase:FBgn0003429

C;Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein

Query Match 37.8%; Score 17; DB 2; Length 13;

Best Local Similarity 75.0%; Pred. No. 3.4e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 7

Db 10 DDLV 13

Search completed: April 6, 2006, 17:04:00
 Job time : 20 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 6, 2006, 16:51:26 ; Search time 116.333 Seconds
(without alignments)
54.582 Million cell updates/sec

Title: US-10-791-217a-2
Perfect score: 45
Sequence: 1 VLHDDLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 7855

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	48.9	12	Q6LAP7_HUMAN	Q6LAP7 homo sapien
2	22	48.9	13	Q6LCH4_RAT	Q6LCH4 rattus norv
3	22	48.9	14	Q95179_HUMAN	Q95179 homo sapien
4	22	48.9	15	Q86TJ6_HUMAN	Q86TJ6 homo sapien
5	22	48.9	15	Q9TWT4_LUTRE	Q9TWT4 lumbricus t
6	21	46.7	11	UF05_MOUSE	UF05 mus musculu
7	21	46.7	11	Q66874_GCALI	Q66874 feline cal
8	21	46.7	11	Q66877_GCALI	Q66877 feline cal
9	21	46.7	15	Q7M063_MOUSE	Q7M063 mus musculu
10	20	44.4	10	F1B8_CERS1	F14337 ceratotheri
11	20	44.4	11	Q47600_ECOLI	Q47600 escherichia
12	20	44.4	12	XYLA_STRVN	P14405 streptomyce
13	20	44.4	15	Q9R5D6_CHRVI	Q9R5D6 chromodium
14	19	42.2	9	Q7R8X5_PLAYO	Q7R8X5 plasmodium
15	19	42.2	9	Q47556_ECOLI	Q47556 escherichia
16	19	42.2	11	Q6LBU0_MOUSE	Q6LBU0 mus musculu
17	19	42.2	13	P82560_STRPY	P82560 streptococc
18	19	42.2	7	Q92B42_STRPY	Q92B42 streptococc
19	19	40.0	14	Q28742_RABIT	Q28742 oryctolagus
20	18	40.0	10	Q718N9_PPAPA	Q718N9 newcastrie d
21	18	40.0	11	Q718K6_PPAPA	Q718K6 newcastrie d
22	18	40.0	12	L1CA_BACST	P83878 bacillus su
23	18	40.0	12	L1CB_BACST	P83879 bacillus su
24	18	40.0	12	L1CB_BACST	P83879 bacillus su
25	18	40.0	12	Q9T2U3_BOVIN	Q9T2U3 bos taurus
26	18	40.0	12	Q9TOY4_BOVIN	Q9TOY4 bos taurus
27	18	40.0	12	Q5MK49_9CIOS	Q5MK49 citrus tris
28	18	40.0	12	Q5MK52_9CIOS	Q5MK52 citrus tris
29	18	40.0	12	Q5MK66_9CIOS	Q5MK66 citrus tris
30	18	40.0	12	Q5MK81_9CIOS	Q5MK81 citrus tris
31	18	40.0	13	Q7YRDL_BISBO	Q7YRDL bison bonas

32	18	40.0	13	2	Q7YR14_BOVIN	Q7YR14 bos taurus
33	18	40.0	13	2	Q7TE19_9CIOS	Q7TE19 citrus tris
34	18	40.0	13	2	Q7TE20_9CIOS	Q7TE20 citrus tris
35	18	40.0	13	2	Q7TE23_9CIOS	Q7TE23 citrus tris
36	18	40.0	13	2	Q7TE26_9CIOS	Q7TE26 citrus tris
37	18	40.0	13	2	Q7TE30_9CIOS	Q7TE30 citrus tris
38	18	40.0	13	2	Q957T7_9PERC	Q957T7 trichopais
39	18	40.0	14	1	SODN_STRGR	P80732 streptomyce
40	18	40.0	14	2	Q8HR43_CLIMI	Q8HR43 clivia minl
41	18	40.0	14	2	Q52840_RHITO	Q52840 rhizobium 1
42	18	40.0	15	1	PSAO_CTCSA	P42032 cucumis sat
43	18	40.0	15	2	Q9UC60_HUMAN	Q9UC60 homo sapien
44	17	37.8	9	2	Q7M355_STRYP	Q7M355 trypanosoma
45	17	37.8	10	2	Q9UMM5_SUISO	Q9UMM5 sulfolobus

ALIGNMENTS

```

RESULT 1
Q6LAP7_HUMAN PRELIMINARY; PRT; 12 AA.
ID Q6LAP7
AC Q6LAP7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Glucose-6-phosphatase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96184388; PubMed=8612793; DOI=10.1016/0014-5793(96)00224-4;
RA Schmolli D., Allan B.B., Burchell A.
RT "Cloning and sequencing of the 5' region of the human glucose-6-
RT phosphatase gene: transcriptional regulation by cAMP, insulin and
RT glucocorticoids in H4IIE hepatoma cells."
RL FEBS Lett. 383:63-66(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Allan Brian B.
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X8937; CA65638.1; -; Genomic_DNA.
FT NON_TER
SQ SEQUENCE 12 AA; 1379 MW; A6B78EEFDE32C446 CRC64;

Query Match 48.9%; Score 22; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. NO. 3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHD 4
   |||
DB 7 VLHD 10

RESULT 2
Q6LCH4_RAT PRELIMINARY; PRT; 13 AA.
ID Q6LCH4
AC Q6LCH4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Glucose-6-phosphatase (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL STRAIN=Sprague-Dawley; TISSUE=Liver;

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RX MEDLINE=97020177; PubMed=8966562;
RA Aiyang D., Zhang Q., Pan W., Maitra S., Pilgis S.J., Lange A.J.;
RT "Regulation of rat liver glucose-6-phosphatase gene expression in
RT different nutritional and hormonal states: gene structure and 5'-
RT flanking sequence.";
RL Diabetes 45:1563-1571 (1996).
DR EMBL; U57552; AB19044.1; -; Genomic_DNA.
FT NON TER 13
SQ SEQUENCE 13 AA; 1591 MW; 0926B8BEFDB32C4 CRC64;

Query Match 48.9%; Score 22; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHD 4
Db 7 VLHD 10

RESULT 3
095179 HUMAN PRELIMINARY; PRT; 14 AA.
AC 095179;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Glucose-6-phosphatase hydrolytic subunit (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99156747; PubMed=10024523; DOI=10.1042/0264-6021:3380457;
RA Schmol D., Maener C., Hinds C.J., Allan B.B., Maltner R.,
RA Burchell A.;
RT "Identification of a cAMP response element within the glucose-6-
RT phosphatase hydrolytic subunit gene promoter which is involved in the
RT transcriptional regulation by cAMP and glucocorticoids in H4IIE
RT hepatoma cells.";
RL Biochem. J. 338:457-463 (1999).
DR EMBL; AF051355; AAD1621.1; -; Genomic_DNA.
FT NON TER 14
SQ SEQUENCE 14 AA; 1666 MW; A6B78BF99F7FD46 CRC64;

Query Match 48.9%; Score 22; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHD 4
Db 9 VLHD 12

RESULT 4
086706 HUMAN PRELIMINARY; PRT; 15 AA.
AC 086706;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE FLJ20097 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Periphereal Nervous System; DOI=10.1073/pnas.242603899;
RX MEDLINE=22388257; PubMed=12477932;
*Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC047757; AAH47757.1; -; mRNA.
SQ SEQUENCE 15 AA; 1843 MW; C309CDBA5B044A3F CRC64;

Query Match 48.9%; Score 22; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHD 4
Db 12 VLHD 15

RESULT 5
097WT4 LUMTB PRELIMINARY; PRT; 15 AA.
AC 097WT4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Hemoglobin (Fragment).
OS Lumbicus terrestris (Common earthworm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Lumbricus.
OX NCBI_TaxID=6398;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93293879; PubMed=8514787;
RA Ownby D.W., Zhu H., Schneider K., Beavis R.C., Chat B.T., Riggs A.F.;
RT "The extracellular hemoglobin of the earthworm, Lumbricus terrestris.
RT Determination of subunit stoichiometry.";
J. Biol. Chem. 268:13539-13547 (1993).
RL J. Biol. Chem. 268:13539-13547 (1993).
SQ SEQUENCE 15 AA; 1665 MW; F9B83FE0050D91F5 CRC64;

Query Match 48.9%; Score 22; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 3.8e+03;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDLID 8
Db 8 HDLID 13

RESULT 6
UF05 MOUSE STANDARD; PRT; 11 AA.
ID UF05_MOUSE
AC P38643;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

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DE Unknown protein from 2D-PAGE of fibroblasts (P48) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins using
 RT preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -1 MISCELLANEOUS; On the 2D-gel the determined pI of this unknown
 CC protein is: 5.5, its MW is: 48 kDa.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC Direct protein sequencing.
 KM NON TER 11
 SQ SEQUENCE 11 AA; 1330 MW; E54835E5CAABAF6A CRC64;

Query Match 46.7%; Score 21; DB 1; Length 11;
 Best Local Similarity 37.5%; Pred. No. 4.2e+03;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VHDDLE 8
 : ||:|
 DB 3 IXDDVIE 10

RESULT 7
 066874_9CALI PRELIMINARY; PRT; 11 AA.
 AC 066874;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Polymerase (Fragment).
 OS Feline calicivirus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Vesivirus.
 NC NCB1_TaxID=11978;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=255;
 RX MEDLINE=95250311; PubMed=7732664;
 RA Seal B.S., Neill J.D.;
 RT "Capsid protein gene sequence of feline calicivirus isolates 255 and
 RT LK; further evidence for capsid protein configuration among feline
 RT caliciviruses.";
 RL Virus Genes 9:183-187(1995).
 DR EMBL; U07130; AAA74412.1; -; Genomic_RNA.
 FT NON TER 1
 SQ SEQUENCE 11 AA; 1232 MW; 4B8B5F5CCABE1E7 CRC64;

Query Match 46.7%; Score 21; DB 2; Length 11;
 Best Local Similarity 57.1%; Pred. No. 4.2e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LHDDLE 8
 |||:
 DB 4 LHDDVIE 10

RESULT 8
 066877_9CALI PRELIMINARY; PRT; 11 AA.
 ID 066877_9CALI PRELIMINARY; PRT; 11 AA.

AC 066877;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Polymerase (Fragment).
 OS Feline calicivirus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Vesivirus.
 NC NCB1_TaxID=11978;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=LLK;
 RX MEDLINE=95250311; PubMed=7732664;
 RA Seal B.S., Neill J.D.;
 RT "Capsid protein gene sequence of feline calicivirus isolates 255 and
 RT LK; further evidence for capsid protein configuration among feline
 RT caliciviruses.";
 RL Virus Genes 9:183-187(1995).
 DR EMBL; U07131; AAA74415.1; -; Genomic_RNA.
 FT NON TER 1
 SQ SEQUENCE 11 AA; 1264 MW; 5B9F43EBCABE1E7 CRC64;

Query Match 46.7%; Score 21; DB 2; Length 11;
 Best Local Similarity 57.1%; Pred. No. 4.2e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LHDDLE 8
 |||:
 DB 4 LHDDVIE 10

RESULT 9
 07M063_MOUSE PRELIMINARY; PRT; 15 AA.
 ID 07M063_MOUSE PRELIMINARY; PRT; 15 AA.
 AC 07M063;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Calnexin (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=94216347; PubMed=8163531;
 RA Lenter M., Vestweber D.;
 RT "The integrin chains beta-1 and alpha-6 associate with the chaperone
 RT calnexin prior to integrin assembly.";
 RL J. Biol. Chem. 269:12263-12268(1994).
 DR PIR; A53594; A53594.
 FT NON TER 1
 SQ SEQUENCE 15 AA; 1693 MW; C62AAA42F9F5F35 CRC64;

Query Match 46.7%; Score 21; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 5.9e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VHDDLE 6
 :|||
 DB 10 IIEDDL 15

RESULT 10
 FIBB_CERST STANDARD; PRT; 10 AA.
 ID FIBB_CERST STANDARD; PRT; 10 AA.
 AC P14537;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-2005 (Rel. 46, Last annotation update)
 DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).

```

GN Name=RGB;
OS Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Rhinocerotidae;
OC Ceratotherium.
OX NCBI_TaxID=9807;
RN [1]
RP PROTEIN SEQUENCE.
RA O'Neil P.B., Doolittle R.F.;
RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL Syst. Zool. 22:590-595(1973).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: Heterohexamer; disulfide linked. Contains 2 sets of 3
CC nonidentical chains (alpha, beta and gamma). The 2 heterotrimers
CC are in head to head conformation with the N-termini in a small
CC central domain (By similarity).
CC -1- DOMAIN: A long coiled coil structure formed by 3 polypeptide
CC chains connects the central module to the C-terminal domains
CC (distal modules). The long C-terminal ends of the alpha chains
CC fold back, contributing a fourth strand to the coiled coil
CC structure.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC InterPro: IPR002181; Fibrinogen_C.
CC DR PROSITE; PS00514; FIBRIN AG_C DOMAIN; PARTIAL.
CC KM Blood coagulation; Coiled coil; Direct protein sequencing; Plasma.
CC PEPTIDE 1 10 Fibrinopeptide B.
CC FT NON_TER 10 10
CC SQ SEQUENCE 10 AA; 1097 MW; 9402B2B2CDDDD33A CRC64;

Query Match 44.4%; Score 20; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDD 5
   |||
Db 1 HDD 3

RESULT 11
Q47600_ECOLI
ID Q47600_ECOLI PRELIMINARY; PRT; 11 AA.
AC Q47600;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rbase protein (Fragment).
DE Name=Rbase;
GN Escherichia coli.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
RT modification systems.";
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL; M63619; AAA24556.1; -, Genomic_DNA.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1232 MW; 63175479572AB5A4 CRC64;

```

```

Query Match 44.4%; Score 20; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 6.6e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LKDDLLA 9
   |||
Db 3 LKSDLLA 10

RESULT 12
ID XYLA_STRVN STANDARD; PRT; 12 AA.
AC P14405;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DR Xylose isomerase (EC 5.3.1.5) (Fragment).
OS Name=xy1A;
OS Streptomyces violaceoruber.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycetaceae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1935;
RN [1]
RP PROTEIN SEQUENCE.
RX STRAIN=LMG 7183;
RX MEDLINE=90104230; PubMed=2604694;
RA Vangryperre W., Ampe C., Kersters-Hilderson H., Tempet P.;
RT "Single active-site histidine in D-xylose isomerase from Streptomyces
RT violaceoruber. Identification by chemical derivatization and peptide
RT mapping.";
RL Biochem. J. 263:195-199(1989).
CC -1- CATALYTIC ACTIVITY: D-xylose = D-xyulose.
CC -1- COFACTOR: Binds 2 magnesium ions per subunit (potential).
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the xylose isomerase family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC HAMAP; MF_00455; -: 1.
CC DR InterPro; IPR001998; Xylose_isom.
CC DR PROSITE; PS00172; XYLOSE_ISOMERASE_1; PARTIAL.
CC DR PROSITE; PS00173; XYLOSE_ISOMERASE_2; PARTIAL.
CC KM Carbohydrate metabolism; Direct protein sequencing; Isomerase;
CC Magnesium; Metal-binding; Pentose shunt; Xylose metabolism.
CC FT ACT_SITE 5 5
CC FT ACT_SITE 8 8 By similarity.
CC FT NON_TER 1 1
CC FT NON_TER 12 12
CC SQ SEQUENCE 12 AA; 1376 MW; E749268EB1AAAA1 CRC64;

Query Match 44.4%; Score 20; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDD 5
   |||
Db 5 HDD 7

RESULT 13
Q9R5D6_CHRYI
ID Q9R5D6_CHRYI PRELIMINARY; PRT; 15 AA.
AC Q9R5D6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE POLY(3-HYDROXYBUTYRIC acid) granule-associated 41 kDa protein

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DE (Fragment).
 OS Chromatium vinosum.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
 OC Chromatiaceae; Allochrochromatium.
 OX NCBI_Taxid=1049;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=93146381; PubMed=1490603; DOI=10.1016/0378-1097(92)90031-I;
 RA Liebergessel M., Schmidt B., Steinhuchel A.;
 RT "Isolation and identification of granule-associated proteins relevant
 for poly(3-hydroxyalkanoic acid) biosynthesis in Chromatium vinosum
 RT D.";
 RL FEMS Microbiol. Lett. 78:227-232(1992).
 SQ SEQUENCE 15 AA; 1874 MW; 165FA9A16BCA2A9D CRC64;

Query Match 44.4%; Score 20; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 9.2e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 HDDDL 8
 :||:|
 Db 8 NDDWLE 13

RESULT 14
 O7R8X5_PLAYO PRELIMINARY; PRT; 9 AA.
 ID O7R8X5_PLAYO PRELIMINARY; PRT; 9 AA.
 AC O7R8X5;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=PY07095;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_Taxid=73239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=17XNL;
 RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Angiluoli S.V., Suh B.B., Koof T.W., Perteau M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shalom S.J., van Aken S.B., Riedmiller S.B., Feldlyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoatibi A., Cummings L.M.,
 RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carnucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 RT parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABU01002528; EAA19452.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 9 AA; 1013 MW; 4684D447244441E7 CRC64;

Query Match 42.2%; Score 19; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLHDDL 6
 :||:|
 Db 1 MLEHNNL 6

RESULT 15
 O47556_ECOLI PRELIMINARY; PRT; 9 AA.
 ID O47556_ECOLI PRELIMINARY; PRT; 9 AA.
 AC O47556;

DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE Aspartate transcarbamoylase regulatory chain (Fragment).
 GN Name=pyrI;
 OS Escherichia coli K12.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_Taxid=83333;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=82275057; PubMed=7051000;
 RA Paua C.D., Karels M.J., Navre M., Schachman H.K.;
 RT "Genes encoding Escherichia coli aspartate transcarbamoylase: the
 RT pyrB-pyrI operon.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:4020-4024(1982).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=83195078; PubMed=6302686;
 RA Hoover T.A., Roof W.D., Foltermann K.F., O'Donovan G.A., Bencini D.A.,
 RA Wild J.R.;
 RT "Nucleotide sequence of the structural gene (pyrB) that encodes the
 RT catalytic polypeptide of aspartate transcarbamoylase of Escherichia
 RT coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2462-2466(1983).
 DR EMBL; J01670; AAA24475.1; -; Genomic_DNA.
 FT NON_TER
 SQ SEQUENCE 9 AA; 1085 MW; 99BFD723344AA1F1 CRC64;

Query Match 42.2%; Score 19; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 HDDDL 8
 :||:|
 Db 3 HDNKLQ 8

Search completed: April 6, 2006, 17:02:58
 Job time : 117.333 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006. Biocooperation Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 17:03:16 ; Search time 27.6667 Seconds
(without alignments)
26.894 Million cell updates/sec

Title: US-10-791-217A-2
Perfect score: 45
Sequence: 1 VLHDDLRA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 186887

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/ECTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	2	US-09-269-250E-20
2	45	100.0	9	2	US-09-489-760-2
3	45	100.0	13	2	US-09-269-250E-28
4	45	100.0	13	2	US-09-489-760-16
5	37	82.2	9	2	US-09-269-250E-18
6	37	82.2	9	2	US-09-489-760-5
7	37	82.2	13	2	US-09-269-250E-26
8	37	82.2	13	2	US-09-489-760-14
9	36	80.0	9	2	US-09-269-250E-29
10	36	80.0	9	2	US-09-489-760-1
11	30	66.7	9	2	US-09-489-760-4
12	28.5	63.3	8	2	US-09-269-250E-38
13	25	55.6	7	2	US-09-025-819-5
14	25	55.6	7	2	US-09-808-126-5
15	25	55.6	7	2	US-09-803-951-5
16	25	55.6	9	2	US-08-582-333A-3
17	25	55.6	9	2	US-09-305-923A-7
18	25	55.6	9	2	US-08-946-298-4
19	24	53.3	10	1	US-08-724-548-20
20	24	53.3	10	1	US-08-724-548-21
21	24	53.3	10	1	US-08-724-548-22
22	24	53.3	10	1	US-08-724-548-23
23	24	53.3	10	1	US-08-724-548-24
24	24	53.3	10	1	US-08-724-548-25
25	24	53.3	10	1	US-08-724-548-26
26	24	53.3	10	2	US-08-159-339A-73
27	24	53.3	10	2	US-07-978-674B-20

28	24	53.3	10	2	US-07-978-674B-21	Sequence 21, Appl
29	24	53.3	10	2	US-07-978-674B-22	Sequence 22, Appl
30	24	53.3	10	2	US-07-978-674B-23	Sequence 23, Appl
31	24	53.3	10	2	US-07-978-674B-24	Sequence 24, Appl
32	24	53.3	10	2	US-07-978-674B-25	Sequence 25, Appl
33	24	53.3	10	2	US-07-978-674B-26	Sequence 26, Appl
34	24	53.3	10	2	US-08-197-484-72	Sequence 72, Appl
35	24	53.3	10	2	US-09-601-729-273	Sequence 723, Appl
36	24	53.3	10	4	PCT-US95-02121-72	Sequence 72, Appl
37	24	53.3	14	1	US-07-909-122-3	Sequence 3, Appl
38	23	51.1	6	2	US-09-217-609A-8	Sequence 8, Appl
39	23	51.1	6	2	US-08-873-235B-8	Sequence 8, Appl
40	23	51.1	9	2	US-08-159-339A-370	Sequence 370, App
41	23	51.1	10	2	US-10-121-857-1	Sequence 1, Appl
42	23	51.1	10	2	US-10-121-857-14	Sequence 14, Appl
43	23	51.1	11	2	US-09-489-156-47	Sequence 47, Appl
44	23	51.1	12	1	US-08-360-784B-32	Sequence 32, Appl
45	23	51.1	12	2	US-09-054-308A-32	Sequence 32, Appl

ALIGNMENTS

```
RESULT 1
US-09-269-250E-20
; Sequence 20, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elia
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-20

Query Match          100.0%; Score 45; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 VLHDDLRA 9
      |||||
Db      1 VLHDDLRA 9

RESULT 2
US-09-489-760-2
; Sequence 2, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leiden
; APPLICANT: Goulmy, Elia A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Histocompatibility antigen
```

US-09-489-760-2

Query Match 100.0%; Score 45; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 V|H|D|D|L|E|A 9
| | | | | | | | |
Db 1 V|H|D|D|L|E|A 9

RESULT 3

US-09-269-250E-28
; Sequence 28, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elise
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Product
US-09-269-250E-28

Query Match 100.0%; Score 45; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 V|H|D|D|L|E|A 9
| | | | | | | | |
Db 3 V|H|D|D|L|E|A 11

RESULT 4

US-09-489-760-16
; Sequence 16, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leiden
; APPLICANT: Goulmy, Elise A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-42850S
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: HA-1+/
US-09-489-760-16

Query Match 100.0%; Score 45; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 V|H|D|D|L|E|A 9
| | | | | | | | |
Db 3 V|H|D|D|L|E|A 11

RESULT 5

US-09-269-250E-18
; Sequence 18, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elise
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-18

Query Match 82.2%; Score 37; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 V|H|D|D|L|E|A 9
| | | | | | | | |
Db 1 V|H|D|D|L|E|A 9

RESULT 6

US-09-489-760-5
; Sequence 5, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leiden
; APPLICANT: Goulmy, Elise A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-42850S
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: KIAA0223 partial complementary DNA
US-09-489-760-5

Query Match 82.2%; Score 37; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 V|H|D|D|L|E|A 9
| | | | | | | | |
Db 1 V|H|D|D|L|E|A 9

RESULT 7

US-09-269-250E-26
; Sequence 26, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elise
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38

SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PCR Product
US-09-269-250E-26

Query Match 82.2%; Score 37; DB 2; Length 13;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLEA 9
|||
3 VLKDDLEA 11

RESULT 8
US-09-489-760-14
Sequence 14, Application US/09489760
Patent No. 6878375
GENERAL INFORMATION:
APPLICANT: Rijkuniversiteit Te Leiden
APPLICANT: Goulmy, Elsa A.J.M
APPLICANT: Hunt, Donald F
APPLICANT: Hard, Victor H
TITLE OF INVENTION: The HA-1 Antigen
FILE REFERENCE: 2183-4285US
CURRENT APPLICATION NUMBER: US/09/489,760
CURRENT FILING DATE: 2000-01-21
EARLIER APPLICATION NUMBER: PCT/NL98/00424
EARLIER FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 13
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: HA-1/-
US-09-489-760-14

Query Match 82.2%; Score 37; DB 2; Length 13;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLEA 9
|||
3 VLKDDLEA 11

RESULT 9
US-09-269-250E-29
Sequence 29, Application US/09269250E
Patent No. 6830883
GENERAL INFORMATION:
APPLICANT: Goulmy, Elsa
TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
FILE REFERENCE: 58994
CURRENT APPLICATION NUMBER: US/09/269,250E
CURRENT FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 9
TYPE: PRT
ORGANISM: Human
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (3)..
OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
US-09-269-250E-29

Query Match 80.0%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLEA 9
|||
3 VLKDDLEA 9

RESULT 10
US-09-489-760-1
Sequence 1, Application US/09489760
Patent No. 6878375
GENERAL INFORMATION:
APPLICANT: Rijkuniversiteit Te Leiden
APPLICANT: Goulmy, Elsa A.J.M
APPLICANT: Hunt, Donald F
APPLICANT: Hard, Victor H
TITLE OF INVENTION: The HA-1 Antigen
FILE REFERENCE: 2183-4285US
CURRENT APPLICATION NUMBER: US/09/489,760
CURRENT FILING DATE: 2000-01-21
EARLIER APPLICATION NUMBER: PCT/NL98/00424
EARLIER FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 9
TYPE: PRT
ORGANISM: Histocompatibility antigen
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (3)
OTHER INFORMATION: AMINO ACID X REPRESENTS A HISTIDINE OR AN ARGININE
US-09-489-760-1

Query Match 80.0%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLEA 9
|||
3 VLKDDLEA 9

RESULT 11
US-09-489-760-4
Sequence 4, Application US/09489760
Patent No. 6878375
GENERAL INFORMATION:
APPLICANT: Rijkuniversiteit Te Leiden
APPLICANT: Goulmy, Elsa A.J.M
APPLICANT: Hunt, Donald F
APPLICANT: Hard, Victor H
TITLE OF INVENTION: The HA-1 Antigen
FILE REFERENCE: 2183-4285US
CURRENT APPLICATION NUMBER: US/09/489,760
CURRENT FILING DATE: 2000-01-21
EARLIER APPLICATION NUMBER: PCT/NL98/00424
EARLIER FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 9
TYPE: PRT
ORGANISM: Histocompatibility antigen
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (2)..
OTHER INFORMATION: AMINO ACIDS X REPRESENT LEUCINE OR ISOLEUCINE
OTHER INFORMATION: RESIDUES

US-09-489-760-4

Query Match 66.7%; Score 30; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VLHDDLEA 9
Db 1 VLHDDXXEA 9

RESULT 12

US-09-269-250E-38
; Sequence 38, Application US/09269250E
; Patent No. 6830893
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elise
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN
US-09-269-250E-38

Query Match 63.3%; Score 28.5; DB 2; Length 8;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 VLHDDLEA 9
Db 1 VLH-DLEA 8

RESULT 13

US-09-025-819-5
; Sequence 5, Application US/09025819
; Patent No. 6225097
; GENERAL INFORMATION:
; APPLICANT: Oyata, Shusei
; APPLICANT: Nishino, Tokuzo
; APPLICANT: Koyama, Tanetoshi
; APPLICANT: Sato, Yoshihiro
; TITLE OF INVENTION: DECAPRENYL DIPHOSPHATE SYNTHETASE GENE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KENTON & KENTON
; STREET: 1500 K Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,819
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE: 17-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Khalilian, Hour1
; REGISTRATION NUMBER: 39,546
; REFERENCE/DOCKET NUMBER: 10235/2
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-220-4200

; TELEFAX: 202-220-4201

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-025-819-5

Query Match 55.6%; Score 25; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDD 5
Db 3 VLHDD 7

RESULT 14

US-09-808-126-5
; Sequence 5, Application US/09808126
; Patent No. 6410280
; GENERAL INFORMATION:
; APPLICANT: Oyata, Shusei
; APPLICANT: Nishino, Tokuzo
; APPLICANT: Koyama, Tanetoshi
; APPLICANT: Sato, Yoshihiro
; TITLE OF INVENTION: DECAPRENYL DIPHOSPHATE SYNTHETASE GENE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KENTON & KENTON
; STREET: 1500 K Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/808,126
; FILING DATE: 08-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/025,819
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Khalilian, Hour1
; REGISTRATION NUMBER: 39,546
; REFERENCE/DOCKET NUMBER: 10235/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-220-4200
; TELEFAX: 202-220-4201
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-808-126-5

Query Match 55.6%; Score 25; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDD 5
; :|||||

Db 3 LHDD 7

RESULT 15

US-09-803-951-5

; Sequence 5, Application US/09803951

; Patent No. 6413761

; GENERAL INFORMATION:

; APPLICANT: Obata, Shusei

; Niehino, Tokuzo

; Koyama, Tanetoshi

; Sato, Yoshihiro

; TITLE OF INVENTION: DECAPRENYL DIPHOSPHATE SYNTHETASE GENE

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: KENYON & KENYON

; STREET: 1500 K Street, N.W.

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/803,951

; FILING DATE: 13-Mar-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/025,819

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Knallian, Hourl

; REGISTRATION NUMBER: 39,546

; REFERENCE/DOCKET NUMBER: 10235/2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-220-4200

; TELEFAX: 202-220-4201

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-803-951-5

Query Match 55.6%; Score 25; DB 2; Length 7;

Best Local Similarity 80.0%; Pred. No. 4.6e+05;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDD 5

Db 3 LHDD 7

Search completed: April 6, 2006, 17:05:28
Job time : 27.6667 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 6, 2006, 17:22:22 ; Search time 96.6667 Seconds
(without alignments)
38.901 Million cell updates/sec

Title: US-10-791-217A-2
Perfect score: 45
Sequence: 1 VLHDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 324073

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBSCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBSCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBSCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBSCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBSCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBSCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	4	US-10-623-176-2
2	45	100.0	9	4	US-10-791-217-2
3	45	100.0	9	5	US-10-861-335-1
4	45	100.0	9	6	US-11-007-740-20
5	45	100.0	10	4	US-10-623-176-43
6	45	100.0	13	4	US-10-623-176-76
7	45	100.0	13	4	US-10-791-217-16
8	45	100.0	13	6	US-11-007-740-28
9	41	91.1	9	4	US-10-623-176-41
10	41	91.1	9	4	US-10-623-176-45
11	37	82.2	9	4	US-10-623-176-10
12	37	82.2	9	4	US-10-623-176-47
13	37	82.2	9	4	US-10-791-217-5
14	37	82.2	9	6	US-11-007-740-18
15	37	82.2	10	4	US-10-623-176-44
16	37	82.2	12	4	US-10-623-176-65
17	37	82.2	13	4	US-10-623-176-74
18	37	82.2	13	4	US-10-791-217-14
19	37	82.2	13	6	US-11-007-740-26
20	36	80.0	9	4	US-10-623-176-1
21	36	80.0	9	4	US-10-623-176-40
22	36	80.0	9	4	US-10-791-217-1
23	36	80.0	9	6	US-11-007-740-29
24	36	80.0	10	4	US-10-623-176-6
25	36	80.0	10	4	US-10-623-176-24
26	36	80.0	13	4	US-10-623-176-54
27	33	73.3	9	4	US-10-623-176-42

28	33	73.3	9	4	US-10-623-176-46	Sequence 46, Appl
29	32	71.1	9	4	US-10-623-176-4	Sequence 4, Appl
30	32	71.1	14	4	US-10-623-176-50	Sequence 50, Appl
31	30	66.7	9	4	US-10-623-176-14	Sequence 14, Appl
32	30	66.7	9	4	US-10-791-217-4	Sequence 4, Appl
33	30	66.7	9	6	US-11-007-740-40	Sequence 40, Appl
34	29	64.4	9	4	US-10-623-176-48	Sequence 48, Appl
35	28.5	63.3	8	4	US-10-623-176-15	Sequence 15, Appl
36	28.5	63.3	8	6	US-11-007-740-38	Sequence 38, Appl
37	28	62.2	9	4	US-10-623-176-23	Sequence 23, Appl
38	28	62.2	9	4	US-10-623-176-38	Sequence 38, Appl
39	28	62.2	9	4	US-10-777-053-95	Sequence 95, Appl
40	28	62.2	10	4	US-10-837-176-95	Sequence 95, Appl
41	28	62.2	10	4	US-10-623-176-7	Sequence 7, Appl
42	28	62.2	13	4	US-10-623-176-64	Sequence 64, Appl
43	27	60.0	9	5	US-10-705-459-280	Sequence 280, App
44	27	60.0	10	4	US-10-623-176-8	Sequence 8, Appl
45	27	60.0	10	4	US-10-702-400-90	Sequence 90, Appl

ALIGNMENTS

```
RESULT 1
US-10-623-176-2
; Sequence 2, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Ele A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-2

Query Match          100.0%; Score 45; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      1  VLHDDLLEA 9
Db      1  VLHDDLLEA 9

RESULT 2
US-10-791-217-2
; Sequence 2, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elea A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Engelhard, Victor H
```

```
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/10/791,217
; PRIOR FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: obtained from histocompatibility antigen
US-10-791-217-2
```

```
Query Match          100.0%; Score 45; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VLAHDDLEA 9
        |||||
Db       1 VLAHDDLEA 9
```

```
RESULT 3
US-10-861-335-1
; Sequence 1, Application US/10861335
; Publication No. US20050031612A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa A.J.M.
; TITLE OF INVENTION: Minor histocompatibility antigen HA-1: target antigen for immunot
; FILE REFERENCE: 2183-6479US
; CURRENT APPLICATION NUMBER: US/10/861,335
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: PCT/NL02/00791
; PRIOR FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: EP 01204704.9
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HA-1 peptide
US-10-861-335-1
```

```
Query Match          100.0%; Score 45; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VLAHDDLEA 9
        |||||
Db       1 VLAHDDLEA 9
```

```
RESULT 4
US-11-007-740-20
; Sequence 20, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 2799/58994-A
; CURRENT APPLICATION NUMBER: US/11/007,740
; CURRENT FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: 09/269,250
; PRIOR FILING DATE: 1999-05-21
```

```
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-20
```

```
Query Match          100.0%; Score 45; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VLAHDDLEA 9
        |||||
Db       1 VLAHDDLEA 9
```

```
RESULT 5
US-10-623-176-43
; Sequence 43, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: (1)..(10)
US-10-623-176-43
```

```
Query Match          100.0%; Score 45; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VLAHDDLEA 9
        |||||
Db       1 VLAHDDLEA 9
```

```
RESULT 6
US-10-623-176-76
; Sequence 76, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
```

```
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: KIAA0223
; OTHER INFORMATION: positive derived from a presumed HA-1 homozygous
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(13)
US-10-623-176-76
```

```
Query Match          100.0%; Score 45; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VLHDDLLEA 9
        |||||
        3 VLHDDLLEA 11
```

```
RESULT 7
US-10-791-217-16
; Sequence 16, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Engelhard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-42850S
; CURRENT APPLICATION NUMBER: US/10/791,217
; PRIOR FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: obtained from HA-1/+ phenotype
US-10-791-217-16
```

```
Query Match          100.0%; Score 45; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VLHDDLLEA 9
        |||||
        3 VLHDDLLEA 11
```

```
RESULT 8
US-11-007-740-28
; Sequence 28, Application US/11007740
; Publication No. US2005023350A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
```

```
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 2799/58994-A
; CURRENT APPLICATION NUMBER: US/11/007,740
; CURRENT FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: 09/269,250
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Product
US-11-007-740-28
```

```
Query Match          100.0%; Score 45; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VLHDDLLEA 9
        |||||
        3 VLHDDLLEA 11
```

```
RESULT 9
US-10-623-176-41
; Sequence 41, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-60470S
; CURRENT APPLICATION NUMBER: US/10/623,176
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-41
```

```
Query Match          91.1%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VLHDDLLE 8
        |||||
        2 VLHDDLLE 9
```

```
RESULT 10
US-10-623-176-45
; Sequence 45, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
```

APPLICANT: Hunt, Donald F.
FILE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-604705
CURRENT FILING DATE: 2003-07-18
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 45
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
NAME/KEY: SITE
LOCATION: (1)..(9)
US-10-623-176-45

Query Match 91.1%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHDDLLEA 9
Db 1 LHDDLLEA 8

RESULT 11
US-10-623-176-10
Sequence 10, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Els A.J.M.
APPLICANT: Hunt, Donald F.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-604705
CURRENT FILING DATE: 2003-07-18
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
NAME/KEY: SITE
LOCATION: (1)..(9)
US-10-623-176-10

Query Match 82.2%; Score 37; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VHDDLLEA 9
Db 1 VHDDLLEA 9

RESULT 12
US-10-623-176-47
Sequence 47, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Els A.J.M.
APPLICANT: Hunt, Donald F.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-604705
CURRENT FILING DATE: 2003-07-18
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
NAME/KEY: SITE
LOCATION: (1)..(9)
US-10-623-176-47

Query Match 82.2%; Score 37; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HHDDLLEA 9
Db 1 HHDDLLEA 7

RESULT 13
US-10-791-217-5
Sequence 5, Application US/10791217
Publication No. US20040191268A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Els A.J.M.
APPLICANT: Hunt, Donald F.
TITLE OF INVENTION: The HA-1 Antigen
FILE REFERENCE: 2183-4285US
CURRENT FILING DATE: 2004-03-02
CURRENT FILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: US/09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: obtained from KIAA0223 partial complementary DNA
US-10-791-217-5

Query Match 82.2%; Score 37; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 82.2%; Score 37; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
|||
Db 1 VLRDDLEA 9

Query Match 82.2%; Score 37; DB 4; Length 10;
Best Local Similarity 88.9%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
|||
Db 1 VLRDDLEA 9

RESULT 14
US-11-007-740-18

; Sequence 18, Application US/11007740
; Publication No. US2005023350A1
; GENERAL INFORMATION:

; APPLICANT: Goulmy, Elis

; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1

; FILE REFERENCE: 2799/58994-A

; CURRENT FILING DATE: 2004-12-08

; PRIOR APPLICATION NUMBER: 09/269,250

; PRIOR FILING DATE: 1999-05-21

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 18

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments

US-11-007-740-18

Query Match 82.2%; Score 37; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
|||
Db 1 VLRDDLEA 9

RESULT 15
US-10-623-176-44

; Sequence 44, Application US/10623176

; Publication No. US20040092446A1

; GENERAL INFORMATION:

; APPLICANT: Goulmy, Elis A.J.M.

; APPLICANT: Hunt, Donald F.

; TITLE OF INVENTION: HA-1 epitopes and uses thereof

; FILE REFERENCE: 2183-6047US

; CURRENT APPLICATION NUMBER: US/10/623,176

; CURRENT FILING DATE: 2003-07-18

; PRIOR APPLICATION NUMBER: 09/489,760

; PRIOR FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: EP 97202303.0

; PRIOR FILING DATE: 1997-07-23

; PRIOR APPLICATION NUMBER: PCT/NL98/00424

; PRIOR FILING DATE: 1998-07-23

; PRIOR APPLICATION NUMBER: JP 2000-504165

; PRIOR FILING DATE: 2000-01-24

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 44

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide

; NAME/KEY: SITE

; LOCATION: (1)..(10)

US-10-623-176-44

Search completed: April 6, 2006, 17:28:45
Job time : 96.6667 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using BW model

Run on: April 6, 2006, 17:24:07 ; Search time 12.6667 Seconds
(without alignments)
22.163 Million cell updates/sec

Title: US-10-791-217a-2

Perfect score: 45
Sequence: 1 VHDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 65691

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*
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2: /SIDSS/ptocdata/2/pubpaa/US06 NEW PUB.pep:*
3: /SIDSS/ptocdata/2/pubpaa/US07 NEW PUB.pep:*
4: /SIDSS/ptocdata/2/pubpaa/PCT_NEW_PUB.pep:*
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7: /SIDSS/ptocdata/2/pubpaa/US11 NEW PUB.pep:*
8: /SIDSS/ptocdata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	7	US-11-010-748A-11 Sequence 11, Appl
2	37	82.2	9	7	US-11-010-748A-12 Sequence 12, Appl
3	26	57.8	6	7	US-11-129-143-163 Sequence 163, Appl
4	26	57.8	6	7	US-11-129-143-164 Sequence 164, Appl
5	26	57.8	6	7	US-11-129-143-165 Sequence 165, Appl
6	26	57.8	6	7	US-11-129-143-166 Sequence 166, Appl
7	25	55.6	6	7	US-11-129-143-161 Sequence 161, Appl
8	25	55.6	6	7	US-11-129-143-162 Sequence 162, Appl
9	24	53.3	8	7	US-11-004-399-1155 Sequence 1155, Ap
10	24	53.3	15	6	US-10-931-251A-13 Sequence 13, Appl
11	23	51.1	6	6	US-10-485-788A-353 Sequence 353, Appl
12	23	51.1	7	6	US-10-485-788A-354 Sequence 354, Appl
13	23	51.1	8	6	US-10-485-788A-355 Sequence 355, Appl
14	23	51.1	9	7	US-11-033-039-785 Sequence 785, Appl
15	23	51.1	9	7	US-11-033-039-809 Sequence 809, Appl
16	23	51.1	13	7	US-11-033-039-800 Sequence 800, Appl
17	23	51.1	13	7	US-11-033-039-821 Sequence 821, Appl
18	23	51.1	14	7	US-11-004-399-3188 Sequence 3188, Ap
19	23	51.1	14	7	US-11-004-399-3210 Sequence 3210, Ap
20	23	51.1	15	7	US-11-166-288-5 Sequence 5, Appl1
21	23	51.1	15	7	US-11-166-288-11 Sequence 11, Appl
22	22	48.9	5	6	US-10-485-788A-352 Sequence 352, Appl
23	22	48.9	5	6	US-10-857-435A-443 Sequence 443, Appl
24	22	48.9	7	6	US-10-982-440-126 Sequence 126, Appl
25	22	48.9	8	7	US-11-045-024-444 Sequence 444, Appl

26	22	48.9	8	7	US-11-045-024-5467 Sequence 5467, Ap
27	22	48.9	8	7	US-11-045-024-7094 Sequence 7094, Ap
28	22	48.9	9	7	US-11-045-024-607 Sequence 607, Appl
29	22	48.9	9	7	US-11-045-024-3715 Sequence 3715, Ap
30	22	48.9	9	7	US-11-045-024-5511 Sequence 5511, Ap
31	22	48.9	9	7	US-11-045-024-12585 Sequence 12585, A
32	22	48.9	9	7	US-11-045-024-14029 Sequence 14029, A
33	22	48.9	10	6	US-10-989-767A-159 Sequence 159, Appl
34	22	48.9	10	6	US-10-989-767A-441 Sequence 441, Appl
35	22	48.9	10	6	US-10-989-767A-547 Sequence 547, Appl
36	22	48.9	10	7	US-11-045-024-61 Sequence 61, Appl
37	22	48.9	10	7	US-11-045-024-761 Sequence 761, Appl
38	22	48.9	10	7	US-11-045-024-762 Sequence 762, Appl
39	22	48.9	10	7	US-11-045-024-3822 Sequence 3822, Ap
40	22	48.9	10	7	US-11-045-024-3823 Sequence 3823, Ap
41	22	48.9	10	7	US-11-045-024-7092 Sequence 7092, Ap
42	22	48.9	10	7	US-11-045-024-7118 Sequence 7118, Ap
43	22	48.9	10	7	US-11-045-024-12588 Sequence 12588, A
44	22	48.9	11	7	US-11-045-024-906 Sequence 906, Appl
45	22	48.9	11	7	US-11-045-024-3923 Sequence 3923, Ap

ALIGNMENTS

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RESULT 1
US-11-010-748A-11
; Sequence 11, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T
US-11-010-748A-11

Query Match          100.0%; Score 45; DB 7; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  VHDDLLEA  9
Db      1  VHDDLLEA  9

RESULT 2
US-11-010-748A-12
; Sequence 12, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
```

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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T C
; OTHER INFORMATION: all epitopes
US-11-010-748A-12

Query Match      82.2%; Score 37; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 VHDDLLEA 9
        :|||||
Db      1 VHDDLLEA 9

RESULT 3
US-11-129-143-163
; Sequence 163, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBLIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Bacillus stearotheophilus
US-11-129-143-163

Query Match      57.8%; Score 26; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LHDDL 6
        :||||
Db      1 IHDDL 5

RESULT 4
US-11-129-143-164
; Sequence 164, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBLIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
```

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; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 164
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-11-129-143-164

Query Match      57.8%; Score 26; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LHDDL 6
        :||||
Db      1 IHDDL 5

RESULT 5
US-11-129-143-165
; Sequence 165, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBLIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 165
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-129-143-165

Query Match      57.8%; Score 26; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LHDDL 6
        :||||
Db      1 IHDDL 5

RESULT 6
US-11-129-143-166
; Sequence 166, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBLIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
; LENGTH: 6
; TYPE: PRT
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; ORGANISM: Haemophilus influenzae
US-11-129-143-166

Query Match 57.8%; Score 26; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0;

QY 2 LHDDL 6
:||||
DB 1 IHDDL 5

RESULT 7

US-11-129-143-161
; Sequence 161, Application US/11129143
; Publication No. US20050266518A1

; GENERAL INFORMATION:

; APPLICANT: BERRY, Alan

; APPLICANT: BRETZEL, Werner

; APPLICANT: HUMBLIN, Markus

; APPLICANT: LOPEZ-ULIBARRI, Rual

; APPLICANT: MAYER, Anne F.

; APPLICANT: YELISEEV, Alexei A.

; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION

; FILE REFERENCE: C38435/121966

; CURRENT APPLICATION NUMBER: US/11/129,143

; CURRENT FILING DATE: 2005-05-13

; NUMBER OF SEQ ID NOS: 197

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 161

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Bradyrhizobium japonicum

Query Match 55.6%; Score 25; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0;

QY 2 LHDDL 6
:||||
DB 1 VHDDL 5

RESULT 8

US-11-129-143-162

; Sequence 162, Application US/11129143

; Publication No. US20050266518A1

; GENERAL INFORMATION:

; APPLICANT: BERRY, Alan

; APPLICANT: BRETZEL, Werner

; APPLICANT: HUMBLIN, Markus

; APPLICANT: LOPEZ-ULIBARRI, Rual

; APPLICANT: MAYER, Anne F.

; APPLICANT: YELISEEV, Alexei A.

; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION

; FILE REFERENCE: C38435/121966

; CURRENT APPLICATION NUMBER: US/11/129,143

; CURRENT FILING DATE: 2005-05-13

; NUMBER OF SEQ ID NOS: 197

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 162

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Rhizobium sp. strain NGR234

Query Match 55.6%; Score 25; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0;

QY 2 LHDDL 6
:||||

DB 1 VHDDL 5

RESULT 9

US-11-004-399-1155

; Sequence 1155, Application US/11004399

; Publication No. US20060053516A1

; GENERAL INFORMATION:

; APPLICANT: Chye, Mee Lee

; APPLICANT: Li, Hong Ye

; APPLICANT: Ramalingam, Sathiskumar

; APPLICANT: Poon, Leo Lit Man

; APPLICANT: Peiris, Joseph Sriyal Malik

; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide

; FILE REFERENCE: 2587/73166/RDK

; CURRENT APPLICATION NUMBER: US/11/004,399

; CURRENT FILING DATE: 2004-12-03

; PRIOR APPLICATION NUMBER: US 60/527,637

; NUMBER OF SEQ ID NOS: 4043

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1155

; LENGTH: 8

; TYPE: PRT

; ORGANISM: SARS-CoV Virus

US-11-004-399-1155

Query Match 53.3%; Score 24; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 LHDD 5
:||||
DB 3 LHDD 6

RESULT 10

US-10-931-251A-13

; Sequence 13, Application US/10931251A

; Publication No. US20060046277A1

; GENERAL INFORMATION:

; APPLICANT: BELYAEV, ALEXANDER SERGEEVICH

; APPLICANT: KOLOKITHAS, ANGELO STEPHEN

; APPLICANT: MONELL, CRAIG ROBERT

; TITLE OF INVENTION: PROTEIN KINASE AND PHOSPHATASE SUBSTRATES AND MULTIPLEX

; FILE REFERENCE: STG-106

; CURRENT APPLICATION NUMBER: US/10/931,251A

; CURRENT FILING DATE: 2004-09-01

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 13

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-931-251A-13

Query Match 53.3%; Score 24; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 LHDD 5
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DB 2 LHDD 5

RESULT 11

US-10-485-788A-353

; Sequence 353, Application US/10485788A

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Publication No. US20050282743A1
GENERAL INFORMATION:
APPLICANT: Lu, Peter S.
APPLICANT: Rabinowitz, Joshua D.
APPLICANT: Schweizer, Johannes
APPLICANT: Carrick, Deanna Marie
APPLICANT: Arbor Vita Corporation
TITLE OF INVENTION: Molecular Interactions in Cells
FILE REFERENCE: 20054-00320US
CURRENT APPLICATION NUMBER: US/10/485,788A
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: US 60/309,841
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/360,061
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: WO PCT/US02/24655
PRIOR FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 353
LENGTH: 6
TYPE: PRT
ORGANISM: Homo sapiens
US-10-485-788A-355

Query Match
Best Local Similarity 51.1%; Score 23; DB 6; Length 6;
Pred. No. 1.4e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VLHDDL 6
Db 1 LVHDDV 6

RESULT 12
US-10-485-788A-354
Sequence 354, Application US/10485788A
Publication No. US20050282743A1
GENERAL INFORMATION:
APPLICANT: Lu, Peter S.
APPLICANT: Rabinowitz, Joshua D.
APPLICANT: Schweizer, Johannes
APPLICANT: Carrick, Deanna Marie
APPLICANT: Arbor Vita Corporation
TITLE OF INVENTION: Molecular Interactions in Cells
FILE REFERENCE: 20054-00320US
CURRENT APPLICATION NUMBER: US/10/485,788A
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: US 60/309,841
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/360,061
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: WO PCT/US02/24655
PRIOR FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 354
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
US-10-485-788A-354

Query Match
Best Local Similarity 51.1%; Score 23; DB 6; Length 7;
Pred. No. 1.4e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VLHDDL 6
Db 2 LVHDDV 7

RESULT 13
US-10-485-788A-355
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Sequence 355, Application US/10485788A
Publication No. US20050282743A1
GENERAL INFORMATION:
APPLICANT: Lu, Peter S.
APPLICANT: Rabinowitz, Joshua D.
APPLICANT: Schweizer, Johannes
APPLICANT: Carrick, Deanna Marie
APPLICANT: Arbor Vita Corporation
TITLE OF INVENTION: Molecular Interactions in Cells
FILE REFERENCE: 20054-00320US
CURRENT APPLICATION NUMBER: US/10/485,788A
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: US 60/309,841
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/360,061
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: WO PCT/US02/24655
PRIOR FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 355
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-10-485-788A-355

Query Match
Best Local Similarity 51.1%; Score 23; DB 6; Length 8;
Pred. No. 1.4e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VLHDDL 6
Db 3 LVHDDV 8

RESULT 14
US-11-033-039-785
Sequence 785, Application US/11033039
Publication No. US20060002947A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2017US01
CURRENT APPLICATION NUMBER: US/11/033,039
CURRENT FILING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: 10/245,871
PRIOR FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 1452
SOFTWARE: PatentIn version 3.3
SEQ ID NO 785
LENGTH: 9
TYPE: PRT
ORGANISM: Zaire ebolavirus
US-11-033-039-785

Query Match
Best Local Similarity 51.1%; Score 23; DB 7; Length 9;
Pred. No. 1.4e+05;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 1 VLHDDLEA 9
Db 1 LTHBSTLKA 9

RESULT 15
US-11-033-039-809
Sequence 809, Application US/11033039
Publication No. US20060002947A1
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; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 809
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Zaire ebolavirus
US-11-033-039-809

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Query Match      51.1%; Score 23; DB 7; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.4e+05;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 VLHDDLLEA 9
       :||: ||:
Db      1 LHESTLKA 9

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Search completed: April 6, 2006, 17:29:30
 Job time : 13.6667 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:50:52 ; Search time 114 Seconds
(without alignments)
34.668 Million cell updates/sec

Title: US-10-791-217a-5

Perfect score: 42

Sequence: 1 VLKDDLLRA 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 770462

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
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5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	42	100.0	9	2	AAW99197	Aaw99197 Minor his
2	42	100.0	9	2	AAW97374	Aaw97374 HA-1 R-al
3	42	100.0	9	8	ADH40334	Adh40334 Human min
4	42	100.0	13	2	AAW99198	Aaw99198 DH cell K
5	42	100.0	13	2	AAW97414	Aaw97414 KIA0223
6	37	88.1	9	2	AAW99196	Aaw99196 Minor his
7	37	88.1	9	2	AAW97375	Aaw97375 HA-1 R-al
8	37	88.1	9	8	ADH40333	Adh40333 Human min
9	37	88.1	13	2	AAW99199	Aaw99199 VR cell K
10	36	85.7	9	2	AAW97415	Aaw97415 KIA0223
11	36	85.7	9	2	AAW99195	Aaw99195 Minor his
12	36	85.7	9	2	AAW97572	Aaw97572 T-cell ep
13	29	69.0	9	8	ADT73023	Adt73023 Human RSV
14	27	64.3	9	2	AAW47427	Aaw47427 Prey1 d1
15	26	61.9	9	8	ADT73650	Adt73650 Human RSV
16	26	61.9	9	8	ADT72767	Adt72767 Human RSV
17	26	61.9	10	4	AAW94234	Aaw94234 Human com
18	26	61.9	10	6	ABP71119	Abp71119 E10 prote
19	26	61.9	15	5	AAW47761	Aaw47761 Ribosomal
20	25	59.5	9	5	AAU71428	Aau71428 Human MHC
21	25	59.5	9	8	ADT72766	Adt72766 Human RSV
22	25	59.5	9	8	ADT73689	Adt73689 Human RSV
23	25	59.5	10	2	AAW73901	Aaw73901 B. forsyth
24	25	59.5	10	8	ADQ26722	Adq26722 Topo V Hh

25	25	59.5	14	8	ADU38989	Adu38989 Mutant S1
26	25	59.5	15	5	ABR07889	Abbr07889 Phosphoen
27	24	57.1	7	4	ABR01550	Abbr01550 Zif268 zi
28	24	57.1	9	7	ADM18256	Adm18256 C trachom
29	24	57.1	9	7	ADM18218	Adm18218 Chlamydia
30	24	57.1	10	6	ABR04849	Abrr04849 Human can
31	24	57.1	11	7	ADD23269	Add23269 Breast ca
32	24	57.1	12	2	AAW64577	Aaw64577 Human Pac
33	24	57.1	12	7	ADD23610	Add23610 Breast ca
34	24	57.1	13	5	ADG66269	Adg66269 Human pro
35	24	57.1	13	5	ADG66272	Adg66272 Human pro
36	24	57.1	13	5	ADG66271	Adg66271 Human pro
37	24	57.1	13	5	ADG66270	Adg66270 Human pro
38	24	57.1	13	7	ADD23767	Add23767 Breast ca
39	24	57.1	14	6	ABG74854	Abg74854 Human GHP
40	24	57.1	14	8	ADR73051	Adr73051 L plantar
41	24	57.1	15	6	ABR30509	Abrr30509 Human can
42	24	57.1	15	6	ABR30940	Abrr30940 Human can
43	24	57.1	15	6	ABR31271	Abrr31271 Human can
44	24	57.1	15	6	ABR30473	Abrr30473 Human can
45	24	57.1	15	6	ABR30612	Abrr30612 Human can

ALIGNMENTS

RESULT 1
AAW99197 standard; peptide; 9 AA.
ID AAW99197
XX
AC AAW99197;
XX
DT 20-MAY-1999 (first entry)
XX
DE Minor histocompatibility antigen HA-1 T-cell epitope #3.
XX
DE Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KM graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KM diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS Homo sapiens.
XX
PN W09905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WC-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
XX (UYLE-) RIJXSUNIV LEIDEN.
XX
XX Goulimy EAJM, Hunt DF, Engelhard VH;
XX
XX WPI; 1999-153312/13.
XX
PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
XX
PS Disclosure; Page 15; 47pp; English.
XX
CC The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 42; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLRDILLEA 9
 Db 1 VLRDILLEA 9

RESULT 2

AAW97374
 ID AAW97374 standard; protein; 9 AA.

AC AAW97374;

DT 13-MAY-1999 (first entry)

DE HA-1 R-allele sequence.

XX Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
 KW R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
 KW severe aplastic anaemia; leukaemia; immune deficiency disease; ss.

OS Homo sapiens.

PN WO9905313-A2.

XX 04-FEB-1999.

PF 23-JUL-1998; 98WO-EP004928.

PR 23-JUL-1997; 97BP-00202303.

PR 02-JUN-1998; 98BP-00870125.

XX (UYLE-) RIJXSUNIV LEIDEN.

PI Goulimy E;

XX WPI; 1999-142960/12.

PT Typing minor histocompatibility antigen HA-1 - by amplifying and
 identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
 of genetic aberrances.

PS Claim 13; Fig 5; 59pp; English.

XX The present sequence represents part of the minor histocompatibility
 CC antigen HA-1 R-allele. The specification describes methods for typing
 CC alleles (preferably the H and R alleles) of the minor histocompatibility
 CC antigen HA-1 in a sample, which comprises detecting polymorphic
 CC nucleotides in the CDNA or genomic nucleic acids of the alleles. The
 CC methods can be used for HA-1 typing for bone marrow transplants, severe
 CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
 CC detection of genetic aberrances. The probes and primers of the invention
 CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
 CC anti-idiotypic B cells and/or T cells and antibodies

XX Sequence 9 AA;

Query Match 100.0%; Score 42; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLRDILLEA 9
 Db 1 VLRDILLEA 9

RESULT 3

ADH40334
 ID ADH40334 standard; peptide; 9 AA.

XX AC ADH40334;

XX 11-MAR-2004 (first entry)

DT Human minor histocompatibility antigen HA-1 T cell epitope.

XX human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
 KW minor histocompatibility antigen; mHAg; T cell epitope.

OS Homo sapiens.

PN WO2003106692-A2.

XX 24-DEC-2003.

PF 13-JUN-2003; 2003WO-BP006251.

PR 13-JUN-2002; 2002BP-00013423.

PA (MERE) MERCK PATENT GMBH.

PI Strittmatter W, Moll H;

DR WPI; 2004-082200/08.

XX Providing allelic variant epitope of protein based on single nucleotide
 PT polymorphism by defining target protein, screening database of protein,
 PT identifying, selecting allelic variant protein, creating variant
 PT epitopes.

PS Disclosure; Page 82; 119pp; English.

XX The invention relates to a novel method for providing epitopes of allelic
 CC variants of antigenic proteins from specific species based on single
 CC nucleotide polymorphism (SNP), by defining target protein/peptide or its
 CC subset, screening database of DNA encoding target protein, identifying,
 CC selecting allelic peptide/protein variants, expression product or its
 CC fragment encoded by DNA sequence having SNP, creating variant epitopes,
 CC selecting epitopes binding to MHC protein. A protein of the invention has
 CC cytotoxic activity, and may have a use in a vaccine. The method is
 CC useful for generating a SNP profile of one or more individuals from a
 CC given species by applying the method for several protein from the
 CC individuals, where the SNP profile was related to disease, preferably
 CC cancer. This is useful for diagnosing a disease in an individual by
 CC generating the SNP-related polymorphic profile. A method of the invention
 CC is useful for transplanting haematopoietic stem cells from a donor to a
 CC recipient and treating cancer, preferably leukaemia, and for determining
 CC the progression, regression or onset of a treated disease. The present
 CC sequence is used in the exemplification of the invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 42; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLRDILLEA 9
 Db 1 VLRDILLEA 9

RESULT 4

AAW9198
 ID AAW9198 standard; peptide; 13 AA.

XX AAW9198;

DT 20-MAY-1999 (first entry)

DE DH cell KIA0223 protein sequence.

XX Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
 KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
 KW diagnosis; aplastic anaemia; immune deficiency disease.

XX Synthetic.
 OS
 XX MO9905174-A1.
 PN
 XX 04-FEB-1999.
 PD
 XX 23-JUL-1998; 98WO-NL000425.
 PF
 XX 23-JUL-1997; 97EP-00202303.
 PR
 XX (UYLE-) RIJKSUNIV LEIDEN.
 PA
 XX Goulmy EAJM, Hunt DF, Engelhard VH;
 PI
 XX WPI; 1999-153312/13.
 DR
 XX N-PSDB; AAX19408.
 PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
 PT diseases and prevent rejection and host versus graft disease in bone
 PT marrow and organ transplantation.
 XX
 PS Disclosure; Page 31; 47pp; English.
 XX
 CC The present invention describes a new peptide (PI) constituting a T-cell
 CC epitope obtainable from the minor histocompatibility antigen HA-1. The
 CC peptide is immunogenic and can be used as part of a vaccine. PI is used
 CC as a medicine, to induce tolerance for transplants, prevent rejection
 CC and/or graft versus host disease, or to treat (auto) immune diseases. In
 CC particular it can be used with bone marrow transplantation, in the
 CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
 CC diseases. The present sequence represents a KIAA0223 sequence given in
 CC the present invention
 XX
 SQ Sequence 13 AA;
 XX
 Query Match 100.0%; Score 42; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VRDDLLAA 9
 DB 3 VRDDLLAA 11
 XX
 RESULT 5
 AAW97414
 ID AAW97414 standard; protein; 13 AA.
 AC
 XX AAW97414;
 XX
 DT 20-MAY-1999 (first entry)
 XX
 DE KIAA0223 polymorphism in HA-1 negative homozygous individuals.
 XX
 KW T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
 KW transplant rejection; Graft-versus-Host Disease; autoimmune disease;
 KW neoplastic haematopoietic cell; KIAA0223 polymorphism.
 XX
 OS Homo sapiens.
 XX
 PN WO9905173-A1.
 XX
 PD 04-FEB-1999.
 XX
 PF 23-JUL-1998; 98WO-NL000424.
 XX
 PR 23-JUL-1997; 97EP-00202303.
 XX
 PA (UYLE-) RIJKSUNIV LEIDEN.
 XX
 PI Goulmy EAJM, Hunt DF, Engelhard VH;
 XX

DR WPI; 1999-142855/12.
 DR N-PSDB; AAX16080.
 XX
 PT Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
 PT for inducing tolerance to transplants and prevent rejection or graft-
 PT versus-host disease.
 XX
 PS Disclosure; Page 38; 57pp; English.
 XX
 CC The present sequence represents the KIAA0223 polymorphism in HA-1
 CC negative homozygous individuals. The specification describes an
 CC immunogenic peptide constituting a T-cell epitope, obtainable from the
 CC minor histocompatibility antigen HA-1. The peptide can be used in
 CC vaccines or pharmaceutical formulations as medicines to induce tolerance
 CC for transplants so as to prevent rejection and/or Graft-versus-Host
 CC Disease, or to treat autoimmune diseases. Neoplastic haematopoietic cells
 CC presenting the peptides, in an HLA class I context, can be eliminated
 CC after specific recognition of the peptides. The peptides can also be used
 CC to raise antibodies, T-cell receptor, B- and T-cells
 XX
 SQ Sequence 13 AA;
 XX
 Query Match 100.0%; Score 42; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VRDDLLAA 9
 DB 3 VRDDLLAA 11
 XX
 RESULT 6
 AAW99196
 ID AAW99196 standard; peptide; 9 AA.
 AC
 XX AAW99196;
 XX
 DT 20-MAY-1999 (first entry)
 XX
 DE Minor histocompatibility antigen HA-1 T-cell epitope #2.
 XX
 KW Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
 KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
 KW diagnosis; aplastic anaemia; immune deficiency disease.
 XX
 OS Homo sapiens.
 XX
 PN WO9905174-A1.
 XX
 PD 04-FEB-1999.
 XX
 PF 23-JUL-1998; 98WO-NL000425.
 XX
 PR 23-JUL-1997; 97EP-00202303.
 XX
 PA (UYLE-) RIJKSUNIV LEIDEN.
 XX
 PI Goulmy EAJM, Hunt DF, Engelhard VH;
 XX
 DR WPI; 1999-153312/13.
 XX
 PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
 PT diseases and prevent rejection and host versus graft disease in bone
 PT marrow and organ transplantation.
 XX
 PS Claim 3; Page 32; 47pp; English.
 XX
 CC The present sequence represents a new peptide (PI) constituting a T-cell
 CC epitope obtainable from the minor histocompatibility antigen HA-1. The
 CC peptide is immunogenic and can be used as part of a vaccine. PI is used
 CC as a medicine, to induce tolerance for transplants, prevent rejection
 CC and/or graft versus host disease, or to treat (auto) immune diseases. In
 CC particular it can be used with bone marrow transplantation, in the

CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
 CC diseases
 XX
 SQ Sequence 9 AA;
 Query Match 88.1%; Score 37; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLKDDLEA 9
 |||||
 1 VLHDDLEA 9

Db 1 VLHDDLEA 9

RESULT 7
 AAM97375
 ID AAM97375 standard; protein; 9 AA.
 XX
 AC AAM97375;
 XX
 DT 13-MAY-1999 (first entry)
 XX
 DE HA-1 H-allele sequence.
 XX
 KM Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
 KM R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
 KM severe aplastic anaemia; leukaemia; immune deficiency disease; 88.
 XX
 OS Homo sapiens.
 XX
 PN WO9905313-A2.
 XX
 PD 04-FEB-1999.
 XX
 PF 23-JUL-1998; 98WO-EP004928.
 XX
 PR 23-JUL-1997; 97EP-00202303.
 PR 02-JUN-1998; 98EP-00870125.
 XX
 PA (UYLE-) RIJXSUNIV LEIDEN.
 XX
 PI Goumy E;
 XX
 DR WPI; 1999-142960/12.
 XX
 PT Typing minor histocompatibility antigen HA-1 - by amplifying and
 PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
 PT of genetic aberrances.
 XX
 PS Claim 18; Fig 5; 59pp; English.
 XX
 CC The present sequence represents part of the minor histocompatibility
 CC antigen HA-1 H-allele. The specification describes methods for typing
 CC alleles (preferably the H and R alleles) of the minor histocompatibility
 CC antigen HA-1 in a sample, which comprise detecting polymorphic
 CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
 CC methods can be used for HA-1 typing for bone marrow transplants, severe
 CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
 CC detection of genetic aberrances. The probes and primers of the invention
 CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
 CC anti-idiotypic B cells and/or T cells and antibodies
 XX
 SQ Sequence 9 AA;
 Query Match 88.1%; Score 37; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLKDDLEA 9
 |||||
 1 VLHDDLEA 9

Db 1 VLHDDLEA 9

RESULT 8
 ADH40333
 ID ADH40333 standard; peptide; 9 AA.
 XX
 AC ADH40333;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Human minor histocompatibility antigen HA-1 T cell epitope.
 XX
 KM human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
 KM minor histocompatibility antigen; mHAg; T cell epitope.
 XX
 OS Homo sapiens.
 XX
 PN WO2003106692-A2.
 XX
 PD 24-DEC-2003.
 XX
 PF 13-JUN-2003; 2003WO-EP006251.
 XX
 PR 13-JUN-2002; 2002EP-00013423.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Strittmatter W, Moll H;
 XX
 DR WPI; 2004-082200/08.
 XX
 PT Providing allelic variant epitope of protein based on single nucleotide
 PT polymorphism by defining target protein, screening database of protein,
 PT identifying, selecting allelic variant protein, creating variant
 PT epitopes.
 XX
 PS Disclosure; Page 82; 119pp; English.
 XX
 CC The invention relates to a novel method for providing epitopes of allelic
 CC variants of antigenic proteins from specific species based on single
 CC nucleotide polymorphism (SNP), by defining target protein/peptide or its
 CC subset, screening database of DNA encoding target protein, identifying,
 CC selecting allelic peptide/protein variants, expression product or its
 CC fragment encoded by DNA sequence having SNP, creating variant epitopes,
 CC selecting epitopes binding to MHC protein. A protein of the invention has
 CC cytostatic activity, and may have a use in a vaccine. The method is
 CC useful for generating a SNP profile of one or more individuals from a
 CC given species by applying the method for several protein from the
 CC individuals, where the SNP profile was related to disease in an individual by
 CC cancer. This is useful for diagnosing a disease in an individual by
 CC generating the SNP-related polymorphic profile. A method of the invention
 CC is useful for transplanting haematopoietic stem cells from a donor to a
 CC recipient and treating cancer, preferably leukaemia, and for determining
 CC the progression, regression or onset of a treated disease. The present
 CC sequence is used in the exemplification of the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 88.1%; Score 37; DB 8; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLKDDLEA 9
 |||||
 1 VLHDDLEA 9

Db 1 VLHDDLEA 9

RESULT 9
 AAM99199
 ID AAM99199 standard; peptide; 13 AA.
 XX
 AC AAM99199;
 XX
 DT 20-MAY-1999 (first entry)
 XX

DE VR cell KIAA0223 protein sequence.
 XX Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
 KM graft versus host disease; bone marrow transplant; leukemia; vaccine;
 KM diagnosis; aplastic anaemia; immune deficiency disease.
 XX Synthetic.
 OS
 XX WO905174-A1.
 PN
 XX 04-FEB-1999.
 PD
 XX 23-JUL-1998; 98WO-NL000425.
 PF
 XX 23-JUL-1997; 97EP-00202303.
 PR
 XX (UYLE-) RIJKSUNIV LEIDEN.
 PA
 XX Goulmy EAJM, Hunt DF, Engelhard VH;
 PI WPI; 1999-153312/13.
 DR N-PSDB; AAX19409.
 XX
 PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
 PT diseases and prevent rejection and host versus graft disease in bone
 PT marrow and organ transplantation.
 PS Disclosure; Page 31; 47pp; English.
 XX
 CC The present invention describes a new peptide (PI) constituting a T-cell
 CC epitope obtainable from the minor histocompatibility antigen HA-1. The
 CC peptide is immunogenic and can be used as part of a vaccine. PI is used
 CC as a medicine, to induce tolerance for transplants, prevent rejection
 CC and/or graft versus host disease, or to treat (auto) immune diseases. In
 CC particular it can be used with bone marrow transplantation, in the
 CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
 CC diseases. The present sequence represents a KIAA0223 sequence given in
 CC the present invention
 CC
 SQ Sequence 13 AA;
 Query Match 88.1%; Score 37; DB 2; Length 13;
 Best Local Similarity 88.9%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VRPDDLEA 9
 |||||
 Db 3 VLHDDLEA 11
 RESULT 10
 AAW97415
 ID AAW97415 standard; protein; 13 AA.
 XX
 AC AAW97415;
 XX
 DT 20-MAY-1999 (first entry)
 XX
 DE KIAA0223 polymorphism in HA-1 positive homozygous individuals.
 XX
 KM T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
 KM transplant rejection; Graft-versus-Host Disease; autoimmune disease;
 KM neoplastic haematopoietic cell; KIAA0223 polymorphism.
 XX
 OS Homo sapiens.
 XX
 PN WO9905173-A1.
 XX
 PD 04-FEB-1999.
 XX
 PF 23-JUL-1998; 98WO-NL000424.
 XX
 PR 23-JUL-1997; 97EP-00202303.
 PT

XX
 PA (UYLE-) RIJKSUNIV LEIDEN.
 XX
 PI Goulmy EAJM, Hunt DF, Engelhard VH;
 XX
 DR WPI; 1999-142855/12.
 DR N-PSDB; AAX16081.
 XX
 PT Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
 PT for inducing tolerance to transplants and prevent rejection or graft-
 PT versus-host disease.
 XX
 PS Disclosure; Page 38; 57pp; English.
 XX
 CC The present sequence represents the KIAA0223 polymorphism in HA-1
 CC positive homozygous individuals. The specification describes an
 CC immunogenic peptide constituting a T-cell epitope, obtainable from the
 CC minor histocompatibility antigen HA-1. The peptide can be used in
 CC vaccines or pharmaceutical formulations as medicines to induce tolerance
 CC for transplants so as to prevent rejection and/or Graft-versus-Host
 CC Disease, or to treat autoimmune diseases. Neoplastic haematopoietic cells
 CC presenting the peptides, in an HLA class I context, can be eliminated
 CC after specific recognition of the peptides. The peptides can also be used
 CC to raise antibodies, T-cell receptor, B- and T-cells
 CC
 SQ Sequence 13 AA;
 Query Match 88.1%; Score 37; DB 2; Length 13;
 Best Local Similarity 88.9%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VRPDDLEA 9
 |||||
 Db 3 VLHDDLEA 11
 RESULT 11
 AAW99195
 ID AAW99195 standard; peptide; 9 AA.
 XX
 AC AAW99195;
 XX
 DT 20-MAY-1999 (first entry)
 XX
 DE Minor histocompatibility antigen HA-1 T-cell epitope #1.
 XX
 KM Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
 KM graft versus host disease; bone marrow transplant; leukemia; vaccine;
 KM diagnosis; aplastic anaemia; immune deficiency disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 FT Key location/Qualifiers
 FT Misc-difference 3 /label= His, Arg
 FT
 XX
 PN WO9905174-A1.
 XX
 PD 04-FEB-1999.
 XX
 PF 23-JUL-1998; 98WO-NL000425.
 XX
 PR 23-JUL-1997; 97EP-00202303.
 XX
 PA (UYLE-) RIJKSUNIV LEIDEN.
 XX
 PI Goulmy EAJM, Hunt DF, Engelhard VH;
 XX
 DR WPI; 1999-153312/13.
 XX
 PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
 PT diseases and prevent rejection and host versus graft disease in bone

PT marrow and organ transplantation.
 XX
 PS Claim 1; Page 32; 47pp; English.
 XX
 CC The present sequence represents a new peptide (P1) constituting a T-cell
 CC epitope obtainable from the minor histocompatibility antigen HA-1. The
 CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
 CC as a medicine, to induce tolerance for transplants, prevent rejection
 CC and/or graft-versus-host disease, or to treat (auto) immune diseases. In
 CC particular it can be used with bone marrow transplantation, in the
 CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
 CC diseases
 XX
 SQ Sequence 9 AA;
 Query Match 85.7%; Score 36; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 1;
 QY 1 VLKDDLEA 9
 DB 1 VLKDDLEA 9
 RESULT 12
 ID AAM97572 standard; peptide; 9 AA.
 AC AAM97572;
 XX
 XX 20-MAY-1999 (first entry)
 DT
 XX T-cell epitope from the minor histocompatibility antigen HA-1.
 DE
 XX T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
 KM transplant rejection; Graft-versus-Host Disease; autoimmune disease;
 KM neoplastic haematopoietic cell.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 3 /note= "His or Arg"
 FT
 XX
 PN W09905173-A1.
 XX
 PD 04-FEB-1999.
 XX
 PF 23-JUL-1998; 98WO-NL000424.
 XX
 PR 23-JUL-1997; 97EP-00202303.
 XX
 PA (UYLE-) RIJXSUNTIV LEIDEN.
 XX
 PI Goulmy EAJM, Hunt DF, Engelhard VH;
 XX
 DR WPI; 1999-142855/12.
 XX
 PT Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
 PT for inducing tolerance to transplants and prevent rejection or graft-
 PT versus-host disease.
 XX
 PS Claim 1; Page 39; 57pp; English.
 XX
 CC The present sequence represents an immunogenic peptide constituting a T-
 CC cell epitope, obtainable from the minor histocompatibility antigen HA-1.
 CC The peptide can be used in vaccines or pharmaceutical formulations as
 CC medicines to induce tolerance for transplants so as to prevent rejection
 CC and/or Graft-versus-Host Disease, or to treat autoimmune diseases.
 CC Neoplastic haematopoietic cells presenting the peptides, in an HLA class
 CC I context, can be eliminated after specific recognition of the peptides.
 CC The peptides can also be used to raise antibodies, T-cell receptor, B-
 CC and T-cells

XX
 SQ Sequence 9 AA;
 Query Match 85.7%; Score 36; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 1;
 QY 1 VLKDDLEA 9
 DB 1 VLKDDLEA 9
 RESULT 13
 ID ADT73023 standard; peptide; 9 AA.
 AC ADT73023;
 XX
 XX 13-JAN-2005 (first entry)
 DT
 XX Human RSV L high affinity binding peptide Segid 919.
 DE
 XX human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
 KM MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.
 XX
 OS Human respiratory syncytial virus.
 OS
 PN W02004092207-A2.
 XX
 PD 28-OCT-2004.
 XX
 PF 16-APR-2004; 2004WO-BP004061.
 XX
 PR 16-APR-2003; 2003BP-0047095.
 XX
 PA (ALGO-) ALGONOMICS NV.
 XX
 PI Lasters I, Deemert J, Stegmann T;
 XX
 DR WPI; 2004-758334/74.
 XX
 PT New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
 PT or P) for inducing an immune response to RSV or for diagnosing,
 PT preventing or treating viral infections, particularly RSV infection.
 XX
 PS Claim 16; SEQ ID NO 919; 143pp; English.
 XX
 CC This invention relates to novel isolated or purified peptides of the
 CC human respiratory syncytial virus (RSV), in particular ten RSV genes
 CC encoding 11 separate viral proteins: non-structural proteins NS-1 (also
 CC known as the IC protein) & NS-2 (1B protein), a polymerase protein L and
 CC eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
 CC SH (also known as the 1A protein). Specifically, it refers to a
 CC composition comprising an above peptide mixed with a pharmaceutical
 CC excipient or an RSV immunogenic composition comprising a recombinant
 CC expression vector with a nucleic acid insert encoding an above peptide.
 CC The present invention describes an in vitro method of detecting cytotoxic
 CC T lymphocytes (CTLs) that respond to a major histocompatibility complex
 CC (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
 CC RSV peptide is useful for preparing a diagnostic composition or an RSV
 CC (prophylactic or therapeutic) vaccine composition for a DNA-based
 CC immunisation, or for preparing an immune response provoking vaccine in
 CC the event of RSV infection (the vaccine being prepared by contacting the
 CC polypeptide in an immune response-provoking amount of specific CTL).
 CC Accordingly, these peptide compositions have virucidal activity. This
 CC peptide sequence is a human RSV high binding affinity peptide of the
 CC invention.
 XX
 SQ Sequence 9 AA;
 Query Match 69.0%; Score 29; DB 8; Length 9;
 Best Local Similarity 44.4%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;
 Matches 4; Conservative 4; Mismatches 1;

QY 1 VLRDDLLLEA 9
 ::|||:
 DB 1 IIRKDDILSA 9

RESULT 14
 ID AAM47427 standard; peptide; 9 AA.
 XX AAM47427;

AC AAM47427;
 DT 05-JUN-1998 (first entry)

XX Prenyl diphosphate synthetase preserved region VI sequence.

KM Prenyl diphosphate synthetase; polyprenyl diphosphate; vitamin K;
 KW ubiquinone; preserved region VI.

OS Synthetic.

XX EP812914-A2.

XX 17-DEC-1997.

XX 13-JUN-1997; 97EP-00109692.

XX 14-JUN-1996; 96JP-00154441.

XX (TOYT) TOYOTA JIDOSHA KK.

PI Muramatsu M, Koike A, Ogura K, Koyama T, Shimizu N, Cho Y;

DR WPI; 1998-034975/04.

PT DNA encoding prenyl diphosphate synthetase subunit(s) - new Micrococcus
 PT prenyl diphosphate synthetase subunit polypeptide(s), and methods for
 PT preparing enzymes from subunit(s).

PS Example 2; Page 26; 46pp; English.

XX The present sequence from preserved region VI of prenyl diphosphate
 CC synthetase (PDS), was used in the preparation of primers for the
 CC amplification of PDS DNA. Substances synthesised by PDS, i.e. polyprenyl
 CC diphosphates, are precursors of physiologically active substances, e.g.
 CC vitamin K and ubiquinones

SQ Sequence 9 AA;

Query Match 64.3%; Score 27; DB 2; Length 9;

Best Local Similarity 57.1%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRRDDLLLE 8
 ::|||:
 DB 3 IIRKDDILSA 9

RESULT 15
 ID ADT73690 standard; peptide; 9 AA.
 XX ADT73690;

AC ADT73690;

DT 13-JAN-2005 (first entry)

XX Human RSV L high affinity binding peptide Segid 1586.

KM human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
 KW MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.

OS Human respiratory syncytial virus.

PN WO2004092207-A2.

XX 28-OCT-2004.

XX 16-APR-2004; 2004WO-EP004061.

XX 16-APR-2003; 2003EP-00447095.

XX (ALGO-) ALGONOMICS NV.

PI Iastere I, Desmet J, Stegmann T;

DR WPI; 2004-758334/74.

PT New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
 PT or P) for inducing an immune response to RSV or for diagnosing,
 PT preventing or treating viral infections, particularly RSV infection.

PS Claim 16; SEQ ID NO 1586; 143pp; English.

XX This invention relates to novel isolated or purified peptides of the
 CC human respiratory syncytial virus (RSV), in particular ten RSV genes
 CC encoding 11 separate viral proteins: non-structural proteins NS-1 (also
 CC known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and
 CC eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
 CC SH (also known as the 1A protein). Specifically, it refers to a
 CC composition comprising an above peptide mixed with a pharmaceutical
 CC excipient or an RSV immunogenic composition comprising a recombinant
 CC expression vector with a nucleic acid insert encoding an above peptide.
 CC The present invention describes an in vitro method of detecting cytotoxic
 CC T lymphocytes (CTLs) that respond to a major histocompatibility complex
 CC (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
 CC RSV peptide is useful for preparing a diagnostic composition or an RSV
 CC immunisation, or for preparing a vaccine composition for a DNA-based
 CC immunisation, or for preparing an immune response provoking vaccine in
 CC the event of RSV infection (the vaccine being prepared by contacting the
 CC polypeptide in an immune response-provoking amount of specific CTL).
 CC Accordingly, these peptide compositions have virucidal activity. This
 CC peptide sequence is a human RSV high binding affinity peptide of the
 CC invention.

SQ Sequence 9 AA;

Query Match 61.9%; Score 26; DB 8; Length 9;

Best Local Similarity 44.4%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLRDDLLLEA 9
 ::|||:
 DB 1 IIRKDDILSA 9

Search completed: April 6, 2006, 16:57:02
 Job time : 114 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 6, 2006, 16:57:26 ; Search time 19 Seconds
(without alignments)
45.576 Million cell updates/sec

Title: US-10-791-217A-5

Perfect score: 42

Sequence: 1 VLRRDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

.Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	50.0	15	2	A53594
2	19.5	46.4	15	2	S62675
3	19	45.2	15	2	E56819
4	18	42.9	10	2	C26997
5	18	42.9	12	2	S65730
6	18	42.9	15	2	S71920
7	18	42.9	15	2	A26997
8	17	40.5	11	2	PH0924
9	17	40.5	11	2	S42449
10	17	40.5	12	2	S39762
11	17	40.5	13	2	PS6043
12	17	40.5	14	2	S50900
13	17	40.5	14	2	C39170
14	17	40.5	15	2	S57584
15	16	38.1	7	2	S68004
16	16	38.1	8	2	PC4131
17	16	38.1	10	2	A61354
18	16	38.1	10	2	S13224
19	16	38.1	12	2	PH1605
20	16	38.1	13	2	S14316
21	16	38.1	13	4	I70075
22	16	38.1	14	2	S29789
23	16	38.1	15	2	B32800
24	16	38.1	15	2	PH1378
25	16	38.1	15	2	PH1377
26	15	35.7	7	2	A59489
27	15	35.7	10	2	F44644
28	15	35.7	11	2	PT0249
29	15	35.7	11	4	S41909

30	15	35.7	13	2	S12388	argA protein - Sal
31	15	35.7	13	2	S65612	tubulin alpha-chain
32	15	35.7	13	2	PC1008	40X extracellular
33	15	35.7	13	2	G44644	neurotoxin-associ
34	15	35.7	14	2	S00316	photosystem I 13K
35	15	35.7	14	2	S57569	T cell receptor V-
36	15	35.7	14	2	A61306	ribonuclease M (EC
37	15	35.7	15	2	P00750	self-incompatibili
38	15	35.7	15	2	PN0629	integration host f
39	15	35.7	15	2	C43334	orf3 J to aacr -
40	15	35.7	15	2	D54226	light-harvesting p
41	14.5	34.5	15	2	D60977	14K protein - Gall
42	14	33.3	7	2	S20446	elastase - Pseudom
43	14	33.3	9	2	A60427	macrophage cytoox
44	14	33.3	10	2	E86128	hypothetical prote
45	14	33.3	11	2	C53652	thR protein - Pse

ALIGNMENTS

```

RESULT 1
A53594
calnexin - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C:Accession: A53594
R:Releer, M.; Vestweber, D.
J. Biol. Chem. 269, 12263-12268, 1994
A>Title: The integrin chains beta-1 and alpha-6 associate with the chaperone calnexin p
A:Reference number: A53594; MUID:94216347; PMID:8163531
A:Accession: A53594
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <LEN>
A:Cross-references: UNIPROT:Q7M063; UNIPARC:UPI000017C62E
C:Keywords: endoplasmic reticulum; molecular chaperone

Query Match
Best Local Similarity 50.0%; Score 21; DB 2; Length 15;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLRRDL 6
DB 10 IIRDDL 15

RESULT 2
S62675
collagen type I - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S62675
R:Mizuno, M.; Kitafima, T.; Tomita, M.; Kuboki, Y.
Biochim. Biophys. Acta 1310, 97-102, 1996
A>Title: The osteoblastic MC3T3-E1 cells synthesized C-terminal propeptide of type I col
A:Reference number: S62675; MUID:97386332; PMID:9244181
A:Accession: S62675
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <MIZ>
A:Cross-references: UNIPROT:Q7M062; UNIPARC:UPI000017C63D

Query Match
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 VLRRDLLE 8
DB 7 VQRRDLLE 15

RESULT 3

```

E56819
PS 1 complex subunit 8 - cucumber (fragment)
C:Species: Cucumis sativus (cucumber)
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C:Accession: E56819
R:Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.
Biochim. Biophys. Acta 1059, 141-148, 1991
A:Title: Characterization of genes that encode subunits of cucumber PS I complex by N-te
A:Reference number: A56819; MUID:91355209; PMID:1883835
A:Accession: E56819
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <IMA>
A:Cross-references: UNIPROT:P42052; UNIPARC:UPI0000132593
A>Note: sequence extracted from NCBI backbone (NCBIP:58606)

Query Match 45.2%; Score 19; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLKDD 5
|:|:|
Db 10 VIQDD 14

RESULT 4
C26997
unspecific monoxygenase (EC 1.14.14.1) isozyme E, phenobarbital-inducible, hepatic - ra
N:Alternate names: cytochrome P450
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-2004
C:Accession: C26997
R:Graves, P.E.; Kaminsky, L.S.; Halpert, J.
Biochemistry 26, 3887-3894, 1987
A:Title: Evidence for functional and structural multiplicity of pregnenolone-16-alpha-ca
A:Reference number: A26997; MUID:88000604; PMID:3651420
A:Accession: C26997
A:Molecule type: protein
A:Residues: 1-10 <GRA>
A:Cross-references: UNIPROT:Q06884; UNIPARC:UPI0000174DA8
C:Superfamily: cytochrome P450 homology
C:Keywords: electron transfer; heme; liver; monoxygenase; oxidoreductase; transmembrane

Query Match 42.9%; Score 18; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 DLLEA 9
|:|:|
Db 2 DLISA 6

RESULT 5
S65730
hemoglobin, extracellular, component - earthworm (Lumbricus terrestris) (fragment)
C:Species: Lumbricus terrestris (common earthworm)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S65730
R:Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
Biochim. Biophys. Acta 1292, 273-280, 1996
A:Title: Characterization of the constituent polypeptides of the extracellular hemoglobi
A:Reference number: S65721; MUID:96176855; PMID:8597573
A:Accession: S65730
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <FUS>
A:Cross-references: UNIPARC:UPI000017BD88

Query Match 42.9%; Score 18; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 RDDLE 8

Db 6 RDHLIQ 11
|:|:|

RESULT 6
S71920
proteinase ECP 32 (EC 3.4.24.-) - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 04-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: S71920
R:Matveyev, V.V.; Usmanova, A.M.; Morozova, A.V.; Collins, J.H.; Khatitina, S.Y.
Biochim. Biophys. Acta 1296, 55-62, 1996
A:Title: Purification and characterization of the proteinase ECP 32 from Escherichia col
A:Reference number: S71920; MUID:96350420; PMID:8765229
A:Accession: S71920
A:Molecule type: protein
A:Residues: 1-15 <MAT>
A:Cross-references: UNIPROT:Q9R4D6; UNIPARC:UPI00000B73DB
A:Experimental source: strain A2
C:Keywords: hydrolase; metalloproteinase

Query Match 42.9%; Score 18; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 2.4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VLKDDL 7
|:|:|
Db 9 VIRDLFL 15

RESULT 7
A26997
unspecific monoxygenase (EC 1.14.14.1) cytochrome P450 2B1, hepatic - rat (fragment)
N:Alternate names: cytochrome P450D
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-2004
C:Accession: A26997
R:Graves, P.E.; Kaminsky, L.S.; Halpert, J.
Biochemistry 26, 3887-3894, 1987
A:Title: Evidence for functional and structural multiplicity of pregnenolone-16-alpha-ca
A:Reference number: A26997; MUID:88000604; PMID:3651420
A:Accession: A26997
A:Molecule type: protein
A:Residues: 1-15 <GRA>
A:Cross-references: UNIPROT:Q06884; UNIPARC:UPI0000174DA7
C:Superfamily: cytochrome P450 homology
C:Keywords: electron transfer; heme; liver; monoxygenase; oxidoreductase; transmembrane

Query Match 42.9%; Score 18; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 DLLEA 9
|:|:|
Db 2 DLISA 6

RESULT 8
PH0924
T-cell receptor beta chain V-D-J region (isolate 10) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0924
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0924
A:Molecule type: mRNA
A:Residues: 1-11 <GOL>
A:Cross-references: UNIPARC:UPI000017C9F3
A:Experimental source: concanavalin A-activated lymphoblast
C:Keywords: T-cell receptor

Query Match 40.5%; Score 17; DB 2; Length 11;
 Best Local Similarity 75.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DILE 8
 |||:
 DB 7 DIME 10

RESULT 9

S42449
 anti protein - phase P7
 C:Species: phase P7
 C>Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
 C:Accession: S42449
 R:Citron, M.; Schuster, H.
 Cell 62, 591-598, 1990
 A>Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.
 A:Reference number: S42448; MUID:90335968; PMID:1696181
 A:Accession: S42449
 A>Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-11 <CIT>
 A:Cross-references: UNIPROT:Q38415; UNIPARC:UPI000009B041; EMBL:M55139; NID:G215705; PMID

Query Match 40.5%; Score 17; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLRDD 6
 |||:
 DB 6 VTRNDI 11

RESULT 10

S39762
 cytochrome P450 UT-7b - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
 C:Accession: S39762
 R:Ohishi, N.; Imaoka, S.; Suzuki, T.; Funae, Y.
 Biochim. Biophys. Acta 1158, 227-236, 1993
 A>Title: Characterization of two P-450 isozymes placed in the rat CYP2D subfamily.
 A:Reference number: S39761; MUID:94072607; PMID:8251521
 A:Accession: S39762
 A:Molecule type: protein
 A:Residues: 1-12 <OHI>
 A:Cross-references: UNIPARC:UPI000017C8F7

Query Match 40.5%; Score 17; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 3e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLRDD 6
 |||:
 DB 3 LIGDDL 8

RESULT 11

PS0443
 potassium channel protein Slo G3 - fruit fly (Drosophila melanogaster) (fragment)
 C:Species: Drosophila melanogaster
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Feb-1997
 C:Accession: PS0443
 R:Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Bond
 Neuron 9, 209-216, 1992
 A>Title: Calcium-activated potassium channels expressed from cloned complementary DNAs.
 A:Reference number: J010697; MUID:92260298; PMID:1497890
 A:Accession: PS0443
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-13 <ADE>

A:Cross-references: UNIPARC:UPI000017BEBA
 C:Comment: This potassium channel is activated by calcium.

C:Genetic: s10
 A:Gene: FlyBase:s10
 A:Cross-references: FlyBase:FBgn003429

Query Match 40.5%; Score 17; DB 2; Length 13;
 Best Local Similarity 75.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 7
 |||:
 DB 10 DDLV 13

RESULT 12

S50900
 chlorophyll a/b-binding protein lhcb5 - spinach (fragment)
 N:Alternate names: light-harvesting complex LHCIIc protein
 C:Species: Spinacia oleracea (spinach)
 C>Date: 19-Mar-1997 #sequence_revision 23-Apr-1999 #text_change 23-Apr-1999
 C:Accession: S50900
 R:Walters, R.G.; Ruban, A.V.; Horton, P.
 Eur. J. Biochem. 226, 1063-1069, 1994
 A>Title: Higher plant light-harvesting complexes LHCIIa and LHCIIc are bound by dicyclo
 A:Reference number: S50900; MUID:95112835; PMID:7813461
 A:Accession: S50900
 A:Molecule type: protein
 A:Residues: 1-14 <NAL>
 A:Cross-references: UNIPARC:UPI000017B182
 C:Superfamily: chlorophyll a/b-binding protein
 C:Keywords: chlorophyll; chloroplast; light-harvesting complex; photosynthesis; photosyn

Query Match 40.5%; Score 17; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RDD 5
 |||:
 DB 10 RDD 12

RESULT 13

C39170
 acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) - avocado (fragments)
 C:Species: Persea americana (avocado)
 C>Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 03-Jun-2002
 C:Accession: C39170
 R:Shanklin, J.; Somerville, C.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2510-2514, 1991
 A>Title: Stearoyl-acyl-carrier-protein desaturase from higher plants is structurally un
 A:Reference number: A39170; MUID:91172837; PMID:2006187
 A:Accession: C39170
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <SHA>
 A:Cross-references: UNIPARC:UPI000017CD5B
 C:Keywords: oxidoreductase

Query Match 40.5%; Score 17; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DILE 8
 |||:
 DB 11 DILE 14

RESULT 14

S57584
 T cell receptor V-D-J junctional alpha chain region - human (fragment)
 C:Species: Homo sapiens (man)

C/Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C/Accession: S57584
R/Burrows, S.R.; Sillins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argact, V.P.
submitted to the EMBL Data Library, June 1995
A/Description: T cell receptor repertoire for a viral epitope in humans is diversified h
A/Reference number: S57494
A/Accession: S57584
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-15 <BUR>
A/Cross-references: UNIPARC:UPI0000116747; EMBL:Z49356; NID:g887466; PIDN:CAA90227.1; PI
C/Keywords: T-cell receptor

Query Match 40.5%; Score 17; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RDD 5
|||
Db 8 RDD 10

RESULT 15
S68004
hucolin, 75K chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C/Accession: S68004
R/Edgar, P.F.
FEBS Lett. 375, 159-161, 1995
A/Title: Hucolin, a new corticosteroid-binding protein from human plasma with structural
A/Reference number: S68004; MUID:96087107; PMID:7498469
A/Accession: S68004
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-7 <EDG>
A/Cross-references: UNIPARC:UPI000017C164

Query Match 38.1%; Score 16; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6
|||
Db 4 DDL 6

Search completed: April 6, 2006, 17:03:59
Job time : 20 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:51:26 ; Search time 116.333 Seconds
(without alignments)

54.582 Million cell updates/sec

Title: US-10-791-217a-5

Perfect score: 42

Sequence: 1 VLKDDLEA 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 7855

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	59.5	11	2	Q47600 ECOLI
2	21	50.0	10	2	Q718N9_9PARA
3	21	50.0	11	1	UF05_MOUSE
4	21	50.0	11	1	Q718K6_9PARA
5	21	50.0	15	1	UC27_MAIZE
6	21	50.0	15	2	Q7M063_MOUSE
7	20	47.6	13	2	P82560_STRPY
8	19.5	46.4	15	2	Q7M062_MOUSE
9	19	45.2	10	2	Q9UMM5_MOUSE
10	19	45.2	11	2	Q9UNL8_HUMAN
11	19	45.2	11	2	Q47602 ECOLI
12	19	45.2	14	2	Q9ZB42_STRPY
13	19	45.2	15	1	PSAO_CTCSA
14	19	45.2	15	2	Q9UC60_HUMAN
15	19	45.2	15	2	Q9UCZ7_HUMAN
16	19	45.2	15	2	Q9TRN6_PIG
17	19	45.2	15	2	Q9RS06_CHRVI
18	18	42.9	8	2	Q7XB03_MAIZE
19	18	42.9	9	2	Q7XBP7_MAIZE
20	18	42.9	12	1	X1YA_STRVN
21	18	42.9	12	2	Q9T2U3_BOVIN
22	18	42.9	12	2	Q9TQV4_BOVIN
23	18	42.9	12	2	Q5MK49_9CIOS
24	18	42.9	12	2	Q5MK52_9CIOS
25	18	42.9	12	2	Q5MK66_9CIOS
26	18	42.9	12	2	Q5MK81_9CIOS
27	18	42.9	13	1	UN02_PIPNS
28	18	42.9	13	2	Q7XB02_MAIZE
29	18	42.9	13	2	Q7TE19_9CIOS
30	18	42.9	13	2	Q7TE20_9CIOS
31	18	42.9	13	2	Q7TE23_9CIOS

32	18	42.9	13	2	Q7TE26_9CIOS	Q7te26 citrus tris
33	18	42.9	13	2	Q7TE30_9CIOS	Q7te30 citrus tris
34	18	42.9	13	2	Q957T7_9PERC	Q957t7 trichopsis
35	18	42.9	14	2	Q7XBP6_MAIZE	Q7xbp6 zea mays (m
36	18	42.9	14	2	Q52840_RHIL0	Q52840 rhizobium 1
37	18	42.9	15	2	Q7XB01_MAIZE	Q7xb01 zea mays (m
38	18	42.9	15	2	Q9R4D6_ECOLI	Q9r4d6 escherichia
39	17	40.5	10	2	Q5S732_9FUNG	Q5s732 glomus cale
40	17	40.5	10	2	Q5S733_9FUNG	Q5s733 glomus geos
41	17	40.5	10	2	Q9TQV4_HORSE	Q9tqv4 e equus cab
42	17	40.5	11	2	Q5IKF0_HUMAN	Q5ikf0 homo sapien
43	17	40.5	11	2	Q38415_BPP7	Q38415 bacterioph
44	17	40.5	12	2	Q9XS31_PIG	Q9xs31 sus scrofa
45	17	40.5	12	2	Q7GCS7_ORYZA	Q7gcs7 oryza sativ

ALIGNMENTS

RESULT 1	
Q47600 ECOLI	
ID Q47600; ECOLI PRELIMINARY; PRT; 11 AA.	
AC Q47600;	
DT 01-NOV-1996 (TREMblrel. 01, Created)	
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)	
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)	
DE Rbase protein (Fragment).	
GN Name=Rbase;	
OS Escherichia coli.	
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
OC Enterobacteriaceae; Escherichia.	
OC NCBI_Taxid=562;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RX MEDLINE=91139577; PubMed=1995588;	
RA Tao T., Bourne J.C., Blumenthal R.M.;	
RT "A family of regulatory genes associated with type II restriction-	
RL modification systems."	
RT J. Bacteriol. 173:1367-1375(1991).	
DR EMBL; M63619; AAA24556.1; -; Genomic_DNA.	
FT NON TER 11 11	
SQ SEQUENCE 11 AA; 1232 MW; 63175479572AB5A4 CRC64;	
Query Match	59.5%; Score 25; DB 2; Length 11;
Best Local Similarity	62.5%; Pred. No. 5.5e+02;
Matches	5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy	2 LRDDLEA 9
Db	3 LRSDLEA 10
RESULT 2	
Q718N9_9PARA PRELIMINARY; PRT; 10 AA.	
ID Q718N9;	
AC Q718N9;	
DT 05-JUL-2004 (TREMblrel. 27, Created)	
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)	
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)	
DE Hemagglutinin-neuraminidase (Fragment).	
OS Newcastle disease virus.	
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;	
OC Paramyxoviridae; Paramyxovirinae; Avulavirinae.	
OC NCBI_Taxid=11176;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RA Gould A.R., Hanson B., Sellick K., Kattenbelt J.A., Mackenzie M.,	
RT "Newcastle disease virus fusion and hemagglutinin-neuraminidase gene	
RT motifs as markers for viral lineage."	
RT Avian Pathol. 32:361-373(2003).	
DR EMBL; AF542884; AAQ11609.1; -; Genomic_DNA.	
FT NON TER 1 1	

SO SEQUENCE 10 AA; 1100 MW; 711806AAA337205B CRC64;

Query Match 50.0%; Score 21; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLKDD 5
: : : :
Db 4 ILKDD 8

RESULT 3

UF05_MOUSE STANDARD; PRT; 11 AA.

AC P38643;
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of fibroblasts (P48) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
[1]
PROTEIN SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Paterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins using
RT preparative two-dimensional gel electrophoresis."
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 5.5, its MW is: 48 kDa.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC Direct protein sequencing.

KW NON_TER 11
SQ SEQUENCE 11 AA; 1330 MW; E54835B5CMAABFA CRC64;

Query Match 50.0%; Score 21; DB 1; Length 11;
Best Local Similarity 37.5%; Pred. No. 3.4e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLKDD 8
: : : :
Db 3 IXKDDVIE 10

RESULT 4

Q718K6_9PARA PRELIMINARY; PRT; 11 AA.

AC Q718K6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hemagglutinin-neuraminidase (Fragment).
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Avulaviruses.
NCBI_Taxid=11176;
[1]
RP NCLECTOTIDE SEQUENCE.
RA "Gould A.R., Hanson E., Selleck K., Katzenbelt J.A., Mackenzie M.,
RA Della-Porta A.J.;
RT "Newcastle disease virus fusion and hemagglutinin-neuraminidase gene
RT motifs as markers for viral lineage."
RL Avian Pathol. 32:361-373(2003).

DR EMBL; AF542917; AAQ11642.1; -; Genomic_DNA.

FT NON_TER 1
SQ SEQUENCE 11 AA; 1313 MW; 710428D6A337205B CRC64;

Query Match 50.0%; Score 21; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLKDD 5
: : : :
Db 5 ILKDD 9

RESULT 5

UC27_MAIZE STANDARD; PRT; 15 AA.

AC P80633;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 688)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoidae; Andropogoneae; Zea.
NCBI_Taxid=4577;
[1]
PROTEIN SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program."
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 6.4, its MW is: 48.4 kDa.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.

CC Maize-2DPAGE; P80633; COLEOPTILE.

DR Gramene; P80633; -.

DR MaizeDB; 123958; -.

FT NON_TER 15
SQ SEQUENCE 15 AA; 1853 MW; CA0E12A5DAEBDC7 CRC64;

Query Match 50.0%; Score 21; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.8e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LRDLLLEA 9
: : : :
Db 5 LRDQVYDA 12

RESULT 6

Q7M063_MOUSE PRELIMINARY; PRT; 15 AA.

AC Q7M063;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Calnexin (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

```
OK NCB1_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=94216347; PubMed=6163531;
RA Lenter M., Vestweber D.;
RT "The integrin chains beta-1 and alpha-6 associate with the chaperone
  calnexin prior to integrin assembly.";
RL J. Biol. Chem. 269:12263-12268(1994).
DR PIR; A53594; A53594.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1693 MW; C62AAAA42P5F35 CRC64;

Query Match
Best Local Similarity 50.0%; Score 21; DB 2; Length 15;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLKDDL 6
DB 10 IREDDL 15

RESULT 7
P82560_STRPY PRELIMINARY; PRT; 13 AA.
AC P82560;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DB 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OK NCB1_TaxID=1314;
RN [1]
RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
RC STRAIN=JRS4;
RA Hogan D.A., Du P., Stevenson T.I., Whittton M., Kilby G.W., Rogers J.,
  Vanbogelen R.A.;
RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
  proteins.";
RL Submitted (MAY-2000) to Swiss-Prot.
CC -1- MASS SPECTROMETRY; MW=30142.85; METHOD=Electrospray.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1464 MW; CFE7DB129CE0C6D9 CRC64;

Query Match
Best Local Similarity 47.6%; Score 20; DB 2; Length 13;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 LKDDLEA 9
DB 1 ITDDVFOA 8

RESULT 8
Q7M062_MOUSE PRELIMINARY; PRT; 15 AA.
AC Q7M062;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Collagen type I (Fragment).
OS Mus musculus (Mouse).
OC Buckyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OK NCB1_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=97386332; PubMed=9244181; DOI=10.1016/0167-4889(95)00151-4;
  Mizuno M., Kitafima T., Tomita M., Kuboki Y.
```

```
RT "The osteoblastic MC3T3-E1 cells synthesized C-terminal propeptide of
  type I collagen, which promoted cell-attachment of osteoblasts.";
RL Biochim. Biophys. Acta 1310:97-102(1996).
DR PIR; S62675; S62675.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1729 MW; DCD8F2FC850E542 CRC64;

Query Match
Best Local Similarity 46.4%; Score 19.5; DB 2; Length 15;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 VLKDDL 8
DB 7 VQDRDILE 15

RESULT 9
Q9UMW5_SULSO PRELIMINARY; PRT; 10 AA.
AC Q9UMW5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DB 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Ribosomal protein L4 (Fragment).
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OK NCB1_TaxID=2287;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92042057; PubMed=1939187;
RA Casiano C., Traut R.R.;
RT "Protein topography of Sulfolobus solfataricus ribosomes by cross-
  linking with 2-iminothiolane. Sso L12e, Sso L10e, and Sso L11e are
  neighbors.";
RL J. Biol. Chem. 266:21578-21583(1991).
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1134 MW; C0336E35EAA33AAD CRC64;

Query Match
Best Local Similarity 45.2%; Score 19; DB 2; Length 10;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 RDDLIR 8
DB 5 KDLSLR 10

RESULT 10
Q9UNL8_HUMAN PRELIMINARY; PRT; 11 AA.
AC Q9UNL8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE APC2 protein (Fragment).
OS Homo sapiens (Human).
GN Name=APC2;
ON Homo sapiens (Human).
OC Buckyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OK NCB1_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Carr I.M., Markham A.F., Colleta P.L., Wei L., Ashkham J., Morrison E.,
  Meredith D.M.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DDJ databases.
DR EMBL; AF110338; AAD29275.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1326 MW; 75881D7BB441EAB4 CRC64;
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Query Match 45.2%; Score 19; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLARD 4
 Db 2 VLARD 5

RESULT 11
 O47602 ECOLI PRELIMINARY; PRT; 11 AA.

AC O47602
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Rhae protein (Fragment).
 GN Name=Rhae;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91139577; PubMed=1995588;
 RA Tao T., Bourne J.C., Blumenthal R.M.;
 RT "A family of regulatory genes associated with type II restriction-
 modification systems."
 RT J. Bacteriol. 173:1367-1375(1991).
 DR EMBL; M63620; AAA24558.1; -; Genomic_DNA.
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1412 MW; 80ABBI90C736DAAA CRC64;

Query Match 45.2%; Score 19; DB 2; Length 11;
 Best Local Similarity 80.0%; Pred. No. 8.5e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 RDDLL 7
 Db 3 RDDOL 7

RESULT 12
 O9ZB42 STRPY PRELIMINARY; PRT; 14 AA.

AC O9ZB42
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE Ssba (Fragment).
 GN Name=sbda;
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus;
 OX NCBI_TaxID=1314;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CS101;
 RA Podbielski A., Woischnik M., Leonard B.A.B., Schmidt K.H.;
 RT "Characterization of nra, a global negative regulator gene in group A
 streptococci."
 RT Mol. Microbiol. 31:0-0(1999).
 DR EMBL; U49397; AAC97153.1; -; Genomic_DNA.
 FT NON TER 1
 SQ SEQUENCE 14 AA; 1618 MW; 47074F277A834F17 CRC64;

Query Match 45.2%; Score 19; DB 2; Length 14;
 Best Local Similarity 57.1%; Pred. No. 1.1e+04;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VLARDLL 7
 Db 6 VLARDTL 12

RESULT 13
 PSAO_CUCSA STANDARD; PRT; 15 AA.

AC P42052;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Photosystem I reaction centre subunit 8 (Photosystem I 17.5 kDa
 protein) (Fragment).
 DE Protein (Fragment).
 GN Name=PSAM;
 OS Cucumis sativus (Cucumber).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucurbit.
 OX NCBI_TaxID=3659;
 RN [1]

RP PROTEIN SEQUENCE.
 RC TISSUE=Cotyledon;
 RX MEDLINE=91355209; PubMed=1883835;
 RA Iwasaki Y., Ishikawa H., Hibino T., Takabe T.;
 RT "Characterization of genes that encode subunits of cucumber PS I
 complex by N-terminal sequencing."
 RT Biochim. Biophys. Acta 1059:141-148(1991).
 CC -!- FUNCTION: Essential for the activity of NADP photoreduction.

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 CC removed.

DR PIR; E56819; E56819.
 KW Chloroplast; Direct protein sequencing; Membrane; Photosynthesis;
 KW Photosystem I; Thylakoid.
 FT NON TER 15
 SQ SEQUENCE 15 AA; 1715 MW; CA0BF5DAD403D9F4 CRC64;

Query Match 45.2%; Score 19; DB 1; Length 15;
 Best Local Similarity 60.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLARD 5
 Db 10 VLIDD 14

RESULT 14
 O9UC60 HUMAN PRELIMINARY; PRT; 15 AA.

AC O9UC60;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE N-acetylmuramyl-L-alanine amidase (EC 3.5.1.28) (Fragment).
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Eureleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP PROTEIN SEQUENCE.
 RX MEDLINE=95392215; PubMed=7663175; DOI=10.1006/prep.1995.1049;
 RA De Pauw P., Neyt C., Vanderwinkel B., Wattiez R., Falmagne P.;
 RT "Characterization of human serum N-acetylmuramyl-L-alanine amidase
 purified by affinity chromatography."
 RT Protein Expr. Purif. 6:371-378(1995).
 DR GO; GO:0008745; R-N-acetylmuramyl-L-alanine amidase activity; TMS.
 DR GO; GO:0001519; Peptide amidation; NMS.

SQ SEQUENCE 15 AA; 1600 MW; 9016B00FF99E780A CRC64;

Query Match 45.2%; Score 19; DB 2; Length 15;

Best Local Similarity 33.3%; Pred. No. 1.2e+04;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 VRDDLLA 9
:|:|:
DB 4 LMDSVIQA 12

RESULT 15

09UC27 HUMAN
ID 09UC27_HUMAN PRELIMINARY; PRT; 15 AA.
AC 09UC27;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, last annotation update)
DE BCL2-interactive cell death susceptibility regulator (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96071131; PubMed=7475270;
RA Meljerink J.P., Smetsers T.F., Sloetjes A.W., Linders E.H.,
RA Mensink B.J.;
RT "Bax mutations in cell lines derived from hematological
malignancies.";
RL Leukemia 9:1828-1832(1995).
SQ SEQUENCE 15 AA; 1860 MW; 4F9238D6FE9743DB CRC64;

Query Match 45.2%; Score 19; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRDDL 6
:|:|:
DB 4 IRDEL 8

Search completed: April 6, 2006, 17:02:57
Job time : 116.333 secs

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US-09-489-760-5

Query Match 100.0%; Score 42; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 VLARDLLEA 9
DB 1 VLARDLLEA 9

RESULT 3

US-09-269-250E-26

; Sequence 26, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Product
US-09-269-250E-26

Query Match 100.0%; Score 42; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.028; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 VLARDLLEA 9
DB 3 VLARDLLEA 11

RESULT 4

US-09-489-760-14

; Sequence 14, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leiden
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: HA-1/-
US-09-489-760-14

Query Match 100.0%; Score 42; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.028; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY * 1 VLARDLLEA 9
DB 3 VLARDLLEA 11

RESULT 5

US-09-269-250E-20

; Sequence 20, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-20

Query Match 88.1%; Score 37; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 1;

QY 1 VLARDLLEA 9
DB 1 VLARDLLEA 9

RESULT 6

US-09-489-760-2

; Sequence 2, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leiden
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Histocompatibility antigen
US-09-489-760-2

Query Match 88.1%; Score 37; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 1;

QY 1 VLARDLLEA 9
DB 1 VLARDLLEA 9

RESULT 7

US-09-269-250E-28

; Sequence 28, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38


```
SOFTWARE: Patentin version 3.1
SEQ ID NO 28
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PCR Product
US-09-269-250E-28
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```
Query Match      88.1%; Score 37; DB 2; Length 13;
Best Local Similarity 88.9%; Pred. No. 0.29;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 VLKDDLEA 9
        |||||||
Db      3 VLKDDLEA 11
```

```
RESULT 8
US-09-489-760-16
Sequence 16, Application US/09489760
GENERAL INFORMATION:
APPLICANT: Rijksuniversiteit Te Leiden
APPLICANT: Goulimy, Elsa A.J.M
APPLICANT: Hunt, Donald F
APPLICANT: Hard, Victor H
TITLE OF INVENTION: The HA-1 Antigen
FILE REFERENCE: 2183-4285US
CURRENT APPLICATION NUMBER: US/09/489,760
CURRENT FILING DATE: 2000-01-21
EARLIER APPLICATION NUMBER: PCT/NL98/00424
EARLIER FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 13
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: HA-1+/-
US-09-489-760-16
```

```
Query Match      88.1%; Score 37; DB 2; Length 13;
Best Local Similarity 88.9%; Pred. No. 0.29;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 VLKDDLEA 9
        |||||||
Db      3 VLKDDLEA 11
```

```
RESULT 9
US-09-269-250E-29
Sequence 29, Application US/09269250E
Patent No. 6830883
GENERAL INFORMATION:
APPLICANT: Goulimy, Elsa
TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
FILE REFERENCE: 58994
CURRENT APPLICATION NUMBER: US/09/269,250E
CURRENT FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 29
LENGTH: 9
TYPE: PRT
ORGANISM: Human
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (3) .. (3)
OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
US-09-269-250E-29
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```
Query Match      85.7%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 VLKDDLEA 9
        |||||||
Db      1 VLKDDLEA 9
```

```
RESULT 10
US-09-489-760-1
Sequence 1, Application US/09489760
Patent No. 6878375
GENERAL INFORMATION:
APPLICANT: Rijksuniversiteit Te Leiden
APPLICANT: Goulimy, Elsa A.J.M
APPLICANT: Hunt, Donald F
APPLICANT: Hard, Victor H
TITLE OF INVENTION: The HA-1 Antigen
FILE REFERENCE: 2183-4285US
CURRENT APPLICATION NUMBER: US/09/489,760
CURRENT FILING DATE: 2000-01-21
EARLIER APPLICATION NUMBER: PCT/NL98/00424
EARLIER FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 9
TYPE: PRT
ORGANISM: Histocompatibility antigen
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (3)
OTHER INFORMATION: AMINO ACID X REPRESENTS A HISTIDINE OR AN ARGININE
US-09-489-760-1
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```
Query Match      85.7%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 VLKDDLEA 9
        |||||||
Db      1 VLKDDLEA 9
```

```
RESULT 11
US-09-217-609A-11
Sequence 11, Application US/09217609A
Patent No. 6071733
GENERAL INFORMATION:
APPLICANT: MURAMATSU, Masayoshi
APPLICANT: KOIKE, Ayumi
APPLICANT: OGURA, Kyoze
APPLICANT: KOTAWA, Taneosshi
APPLICANT: SHIMIZU, Naoto
APPLICANT: CHO, Yemwin
TITLE OF INVENTION: Prenyl Diphosphate Synthetase Genes
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSES: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, NW - Suite 600
CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: Wordperfect 6.1 for Windows
CURRENT APPLICATION DATA:
```

```

; APPLICATION NUMBER: US/09/217,609A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/873,235
; FILING DATE: 11-Jun-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: TOFFENETTI, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 10235/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-1776
; TELEFAX: 202-429-0796
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-217-609A-11

Query Match          64.3%; Score 27; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.6e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 LRDDLE 8
Db      3 IRDDILD 9

RESULT 12
US-08-873-235B-11
; Sequence 11, Application US/08873235B
; Patent No. 6174715
; GENERAL INFORMATION:
; APPLICANT: MURAMATSU, Masayoshi
; APPLICANT: KOIKE, Ayumi
; APPLICANT: OGURA, Kyozo
; APPLICANT: KOYAMA, Tanetoshi
; APPLICANT: SHIMIZU, Naoto
; APPLICANT: CHO, Yewwin
; TITLE OF INVENTION: Prenyl Diphosphate Synthetase Genes
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, NW - Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: US
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
; SOFTWARE: Wordperfect 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,235B
; FILING DATE: 11-Jun-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 154441/1996
; FILING DATE: 14-Jun-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: TOFFENETTI, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 10235/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-1776
; TELEFAX: 202-429-0796
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
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```

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-873-235B-11

Query Match          64.3%; Score 27; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.6e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 LRDDLE 8
Db      3 IRDDILD 9

RESULT 13
US-09-269-250E-38
; Sequence 38, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Gouilly, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN
; US-09-269-250E-38

Query Match          54.8%; Score 23; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 DLLEA 9
Db      4 DLLEA 8

RESULT 14
US-09-972-115A-64
; Sequence 64, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-972-115A-64

Query Match          54.8%; Score 23; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 RDDLLE 8
Db      5 KDDLLE 10
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RESULT 15
US-08-962-284-8
; Sequence 8, Application US/08962284
; Patent No. 5985608
; GENERAL INFORMATION:
; APPLICANT: Luna, Elizabeth J.
; APPLICANT: Pestonjansp, Kerst N.
; APPLICANT: Pope, Robert K.
; APPLICANT: Wulfkuhle, Julia D.
; TITLE OF INVENTION: ACTIN-BINDING POLYPEPTIDES
; TITLE OF INVENTION: AND NUCLEIC ACIDS ENCODING THE SAME
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/962,284
; FILING DATE: 31-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, Peter J.
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 07917/058001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-962-284-8

Query Match 54.8%; Score 23; DB 1; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0;
Gaps 0;

QY 3 RDDLE 8
|:|:|:
Db 6 REDLLQ 11

Search completed: April 6, 2006, 17:05:28
Job time : 28.6667 secs

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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: April 6, 2006, 17:22:22 ; Search time 96.6667 Seconds
(without alignments)
38.901 Million cell updates/sec

Title: US-10-791-217a-5
Perfect score: 42
Sequence: 1 VLRDILEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 324073

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	9	4	US-10-623-176-10 Sequence 10, Appl
2	42	100.0	9	4	US-10-791-217-5 Sequence 5, Appl
3	42	100.0	9	6	US-11-007-740-18 Sequence 18, Appl
4	42	100.0	10	4	US-10-623-176-44 Sequence 44, Appl
5	42	100.0	12	4	US-10-623-176-65 Sequence 65, Appl
6	42	100.0	13	4	US-10-623-176-74 Sequence 74, Appl
7	42	100.0	13	4	US-10-791-217-14 Sequence 14, Appl
8	42	100.0	13	6	US-11-007-740-26 Sequence 26, Appl
9	38	90.5	9	4	US-10-623-176-42 Sequence 42, Appl
10	38	90.5	9	4	US-10-623-176-46 Sequence 46, Appl
11	37	88.1	9	4	US-10-623-176-2 Sequence 2, Appl
12	37	88.1	9	4	US-10-791-217-2 Sequence 1, Appl
13	37	88.1	9	5	US-10-861-335-1 Sequence 20, Appl
14	37	88.1	9	6	US-11-007-740-20 Sequence 43, Appl
15	37	88.1	10	4	US-10-623-176-43 Sequence 76, Appl
16	37	88.1	13	4	US-10-623-176-76 Sequence 16, Appl
17	37	88.1	13	4	US-10-791-217-16 Sequence 28, Appl
18	37	88.1	13	6	US-11-007-740-28 Sequence 1, Appl
19	36	85.7	9	4	US-10-623-176-1 Sequence 29, Appl
20	36	85.7	9	4	US-10-791-217-1 Sequence 24, Appl
21	36	85.7	9	6	US-11-007-740-29 Sequence 48, Appl
22	34	81.0	10	4	US-10-623-176-24 Sequence 23, Appl
23	34	81.0	9	4	US-10-623-176-48 Sequence 41, Appl
24	33	78.6	9	4	US-10-623-176-23 Sequence 45, Appl
25	33	78.6	9	4	US-10-623-176-41 Sequence 7, Appl
26	33	78.6	9	4	US-10-623-176-45 Sequence 10, Appl
27	33	78.6	10	4	US-10-623-176-7 Sequence 10, Appl

28	33	78.6	13	4	US-10-623-176-64 Sequence 64, Appl
29	29	69.0	9	4	US-10-623-176-5 Sequence 5, Appl
30	29	69.0	9	4	US-10-623-176-47 Sequence 47, Appl
31	29	69.0	14	4	US-10-623-176-62 Sequence 62, Appl
32	28	66.7	9	4	US-10-623-176-40 Sequence 40, Appl
33	28	66.7	10	4	US-10-623-176-6 Sequence 6, Appl
34	28	66.7	13	4	US-10-623-176-54 Sequence 54, Appl
35	27	64.3	10	4	US-10-623-176-8 Sequence 8, Appl
36	26	61.9	10	3	US-09-572-404B-428 Sequence 428, App
37	26	61.9	10	4	US-10-153-344-11 Sequence 11, Appl
38	25	59.5	9	3	US-09-834-765-349 Sequence 349, App
39	25	59.5	9	4	US-10-623-176-39 Sequence 39, Appl
40	25	59.5	10	4	US-10-702-400-90 Sequence 90, Appl
41	25	59.5	10	5	US-10-805-650-90 Sequence 90, Appl
42	24	57.1	7	4	US-10-271-708-16 Sequence 16, Appl
43	24	57.1	9	4	US-10-623-176-4 Sequence 4, Appl
44	24	57.1	9	5	US-10-503-135-26 Sequence 26, Appl
45	24	57.1	9	5	US-10-503-135-64 Sequence 64, Appl

ALIGNMENTS

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RESULT 1
US-10-623-176-10
; Sequence 10, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Elia A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-10

Query Match          100.0%; Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLRDILEA 9
DB      1 VLRDILEA 9

RESULT 2
US-10-791-217-5
; Sequence 5, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Elia A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H
```

```
/ TITLE OF INVENTION: The HA-1 Antigen
/ FILE REFERENCE: 2183-4285US
/ CURRENT APPLICATION NUMBER: US/10/791,217
/ CURRENT FILING DATE: 2004-03-02
/ PRIOR APPLICATION NUMBER: US/09/489,760
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: PCT/NL98/00424
/ PRIOR FILING DATE: 1998-07-23
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: obtained from KIAA0223 partial complementary DNA
US-10-791-217-5
```

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Query Match          100.0%; Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 VRDDLEA 9
   |||||
Db 1 VRDDLEA 9
```

```
RESULT 3
US-11-007-740-18
/ Sequence 18, Application US/11007740
/ Publication No. US2005023350A1
/ GENERAL INFORMATION:
/ APPLICANT: Goulimy, Els
/ TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
/ FILE REFERENCE: 2799/58994-A
/ CURRENT APPLICATION NUMBER: US/11/007,740
/ CURRENT FILING DATE: 2004-12-08
/ PRIOR APPLICATION NUMBER: 09/269,250
/ PRIOR FILING DATE: 1999-05-21
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 18
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-18
```

```
Query Match          100.0%; Score 42; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VRDDLEA 9
   |||||
Db 1 VRDDLEA 9
```

```
RESULT 4
US-10-623-176-44
/ Sequence 44, Application US/10623176
/ Publication No. US20040092446A1
/ GENERAL INFORMATION:
/ APPLICANT: Goulimy, Els A.J.M.
/ APPLICANT: Hunt, Donald F.
/ APPLICANT: Engelhard, Victor H.
/ TITLE OF INVENTION: HA-1 epitopes and uses thereof
/ FILE REFERENCE: 2183-6047US
/ CURRENT APPLICATION NUMBER: US/10/623,176
/ CURRENT FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: 09/489,760
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: EP 97202303.0
```

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/ PRIOR FILING DATE: 1997-07-23
/ PRIOR APPLICATION NUMBER: PCT/NL98/00424
/ PRIOR FILING DATE: 1998-07-23
/ PRIOR APPLICATION NUMBER: JP 2000-504165
/ PRIOR FILING DATE: 2000-01-24
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 44
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
/ NAME/KEY: SITE
/ LOCATION: (1)..(10)
US-10-623-176-44
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```
Query Match          100.0%; Score 42; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VRDDLEA 9
   |||||
Db 1 VRDDLEA 9
```

```
RESULT 5
US-10-623-176-65
/ Sequence 65, Application US/10623176
/ Publication No. US20040092446A1
/ GENERAL INFORMATION:
/ APPLICANT: Goulimy, Els A.J.M.
/ APPLICANT: Hunt, Donald F.
/ APPLICANT: Engelhard, Victor H.
/ TITLE OF INVENTION: HA-1 epitopes and uses thereof
/ FILE REFERENCE: 2183-6047US
/ CURRENT APPLICATION NUMBER: US/10/623,176
/ CURRENT FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: 09/489,760
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: EP 97202303.0
/ PRIOR FILING DATE: 1997-07-23
/ PRIOR APPLICATION NUMBER: PCT/NL98/00424
/ PRIOR FILING DATE: 1998-07-23
/ PRIOR APPLICATION NUMBER: JP 2000-504165
/ PRIOR FILING DATE: 2000-01-24
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 65
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
/ NAME/KEY: SITE
/ LOCATION: (1)..(12)
US-10-623-176-65
```

```
Query Match          100.0%; Score 42; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VRDDLEA 9
   |||||
Db 2 VRDDLEA 10
```

```
RESULT 6
US-10-623-176-74
/ Sequence 74, Application US/10623176
/ Publication No. US20040092446A1
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```
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: KIAA0223
; OTHER INFORMATION: sequence derived from a presumed HA-1 negative
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(13)
US-10-623-176-74
```

```
Query Match          100.0%; Score 42; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VLRDDLEA 9
        |||||
Db      3 VLRDDLEA 11

RESULT 7
US-10-791-217-14
; Sequence 14, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/10/791,217
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: obtained from HA-1/- phenotype
US-10-791-217-14
```

```
Query Match          100.0%; Score 42; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLRDDLEA 9
        |||||
Db      3 VLRDDLEA 11
```

```
RESULT 8
US-11-007-740-26
; Sequence 26, Application US/11007740
; Publication No. US2005023350A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 2799/58994-A
; CURRENT APPLICATION NUMBER: US/11/007,740
; CURRENT FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: 09/269,250
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Product
US-11-007-740-26
```

```
Query Match          100.0%; Score 42; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VLRDDLEA 9
        |||||
Db      3 VLRDDLEA 11
```

```
RESULT 9
US-10-623-176-42
; Sequence 42, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-42
```

```
Query Match          90.5%; Score 38; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLRDDLE 8
        |||||
Db      2 VLRDDLE 9
```

```
RESULT 10
US-10-623-176-46
; Sequence 46, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: (1)..(9)
; US-10-623-176-46

Query Match      90.5%; Score 38; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      2 LRDDLLLEA 9
Db      1 LRDDLLLEA 8

RESULT 11
US-10-623-176-2
; Sequence 2, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: (1)..(9)
; US-10-623-176-2
```

```
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-2

Query Match      88.1%; Score 37; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      1 VLRDDLLLEA 9
Db      1 VLHDDLLLEA 9

RESULT 12
US-10-791-217-2
; Sequence 2, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/10/791,217
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: obtained from histocompatibility antigen
; US-10-791-217-2

Query Match      88.1%; Score 37; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      1 VLRDDLLLEA 9
Db      1 VLHDDLLLEA 9

RESULT 13
US-10-861-335-1
; Sequence 1, Application US/10861335
; Publication No. US20050031612A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa A.J.M.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: Minor histocompatibility antigen HA-1: target antigen for immunor
; FILE REFERENCE: 2183-6479US
; CURRENT APPLICATION NUMBER: US/10/861,335
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: PCT/NL02/00791
; PRIOR FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: EP 01204704.9
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HA-1 peptide
; US-10-861-335-1
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Query Match 88.1%; Score 37; DB 5; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLLA 9
|||
1 VLHDDLLA 9

RESULT 14
US-11-007-740-20

; Sequence 20, Application US/11007740
; Publication No. US2005023350A1
; GENERAL INFORMATION:

; APPLICANT: Goulmy, Elsa

; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1

; FILE REFERENCE: 2799/58994-A

; CURRENT APPLICATION NUMBER: US/11/007,740

; CURRENT FILING DATE: 2004-12-08

; PRIOR APPLICATION NUMBER: 09/269,250

; PRIOR FILING DATE: 1999-05-21

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 20

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments

US-11-007-740-20

Query Match

Best Local Similarity 88.1%; Score 37; DB 6; Length 9;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLLA 9
|||
1 VLHDDLLA 9

RESULT 15
US-10-623-176-43

; Sequence 43, Application US/10623176

; Publication No. US20040092446A1

; GENERAL INFORMATION:

; APPLICANT: Goulmy, Elsa A.J.M.

; APPLICANT: Hunt, Donald F.

; TITLE OF INVENTION: HA-1 epitopes and uses thereof

; FILE REFERENCE: 2183-6047US

; CURRENT APPLICATION NUMBER: US/10/623,176

; CURRENT FILING DATE: 2003-07-18

; PRIOR APPLICATION NUMBER: 09/489,760

; PRIOR FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: EP 97202303.0

; PRIOR FILING DATE: 1997-07-23

; PRIOR APPLICATION NUMBER: PCT/NL98/00424

; PRIOR FILING DATE: 1998-07-23

; PRIOR APPLICATION NUMBER: JP 2000-504165

; PRIOR FILING DATE: 2000-01-24

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 43

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide

; NAME/KEY: SITE

; LOCATION: (1)..(10)

US-10-623-176-43

Query Match 88.1%; Score 37; DB 4; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLLA 9
|||
1 VLHDDLLA 9

Search completed: April 6, 2006, 17:28:45
Job time : 96.6667 secs

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OM protein - protein search, using sw model

Run on: April 6, 2006, 17:24:07 ; Search time 12.6667 Seconds
(without alignments)
22.163 Million cell updates/sec

Title: US-10-791-217A-5
Perfect score: 42
Sequence: 1 VLRRDLRA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

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Maximum Match 100%
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3: /SIDSS/prodata/2/pubppa/US07 NEW PUB.pep:*
4: /SIDSS/prodata/2/pubppa/US09 NEW PUB.pep:*
5: /SIDSS/prodata/2/pubppa/US10 NEW PUB.pep:*
6: /SIDSS/prodata/2/pubppa/US11 NEW PUB.pep:*
7: /SIDSS/prodata/2/pubppa/US60 NEW PUB.pep:*
8: /SIDSS/prodata/2/pubppa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	9	US-11-010-748A-12	Sequence 12, Appl
2	37	88.1	9	US-11-010-748A-11	Sequence 11, Appl
3	31	50.0	4	US-11-019-027-17	Sequence 17, Appl
4	21	50.0	7	US-11-096-706-52	Sequence 52, Appl
5	21	50.0	7	US-11-225-686-208	Sequence 208, Appl
6	21	50.0	7	US-11-225-686-211	Sequence 211, Appl
7	21	50.0	7	US-11-225-686-216	Sequence 216, Appl
8	21	50.0	7	US-11-202-009-208	Sequence 208, Appl
9	21	50.0	7	US-11-202-009-211	Sequence 211, Appl
10	21	50.0	7	US-11-202-009-216	Sequence 216, Appl
11	21	50.0	6	US-10-989-767A-219	Sequence 219, Appl
12	21	50.0	6	US-10-989-767A-155	Sequence 155, Appl
13	21	50.0	10	US-10-989-767A-169	Sequence 169, Appl
14	21	50.0	10	US-10-989-767A-268	Sequence 268, Appl
15	21	50.0	10	US-10-989-767A-272	Sequence 272, Appl
16	21	50.0	10	US-10-989-767A-441	Sequence 441, Appl
17	21	50.0	6	US-10-989-767A-547	Sequence 547, Appl
18	20	47.6	5	US-11-129-143-168	Sequence 168, Appl
19	20	47.6	5	US-11-129-143-169	Sequence 169, Appl
20	20	47.6	5	US-11-129-143-170	Sequence 170, Appl
21	20	47.6	5	US-11-129-143-171	Sequence 171, Appl
22	20	47.6	5	US-11-129-143-172	Sequence 172, Appl
23	20	47.6	5	US-11-129-143-173	Sequence 173, Appl
24	20	47.6	7	US-10-982-440-126	Sequence 126, Appl
25	20	47.6	7	US-11-096-706-88	Sequence 88, Appl

26	20	47.6	7	US-11-096-706-164	Sequence 164, Appl
27	20	47.6	8	US-11-021-305-62	Sequence 62, Appl
28	20	47.6	8	US-11-021-305-65	Sequence 65, Appl
29	20	47.6	8	US-11-021-305-66	Sequence 66, Appl
30	20	47.6	9	US-10-927-435-63	Sequence 63, Appl
31	20	47.6	9	US-10-927-435-63	Sequence 63, Appl
32	20	47.6	10	US-11-254-419-60	Sequence 60, Appl
33	20	47.6	10	US-11-254-419-67	Sequence 67, Appl
34	20	47.6	12	US-11-004-399-1909	Sequence 1909, Appl
35	20	47.6	14	US-11-127-677-130	Sequence 130, Appl
36	20	47.6	15	US-10-353-783-71	Sequence 71, Appl
37	20	47.6	15	US-10-718-264-162	Sequence 162, Appl
38	20	47.6	15	US-10-718-264-162	Sequence 162, Appl
39	20	47.6	15	US-10-522-297-112	Sequence 112, Appl
40	20	47.6	15	US-10-522-297-112	Sequence 112, Appl
41	20	47.6	15	US-11-106-932-84	Sequence 84, Appl
42	20	47.6	15	US-11-126-841A-8	Sequence 8, Appl
43	20	47.6	15	US-11-172-740-1404	Sequence 1404, Appl
44	19	45.2	7	US-11-225-686-2954	Sequence 2954, Appl
45	19	45.2	7	US-11-225-686-3877	Sequence 3877, Appl

ALIGNMENTS

RESULT 1
US-11-010-748A-12
Sequence 12, Application US/11010748A
Publication No. US20050244421A1
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMAYER, Wolfgang
APPLICANT: MOILL, Heidemund
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
FILE REFERENCE: MER-136
CURRENT APPLICATION NUMBER: US/11/010,748A
PRIOR FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/EP03/06251
PRIOR FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: EP02013423.5
PRIOR FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 926
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(9)
OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
US-11-010-748A-12

Query Match 100.0%; Score 42; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLRRDLRA 9
DB 1 VLRRDLRA 9

RESULT 2
US-11-010-748A-11
Sequence 11, Application US/11010748A
Publication No. US20050244421A1
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMAYER, Wolfgang
APPLICANT: MOILL, Heidemund
APPLICANT: SCHARM, Burkhard

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
; OTHER INFORMATION: ell epitopes
US-11-010-748A-11

Query Match      88.1%; Score 37; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      1 RDDLLEA 9
DB      1 VLHDDLLEA 9

RESULT 3
US-11-019-027-17
; Sequence 17, Application US/11019027
; Publication No. US20050282181A1
; GENERAL INFORMATION:
; APPLICANT: VAN, Wei
; APPLICANT: SHEN, Wenyan
; APPLICANT: ZHOU, Hongxing
; APPLICANT: ZHOU, Chen
; APPLICANT: COSMAN, David J.
; APPLICANT: CARTER, Paul
; APPLICANT: MARTIN, Francis H.
; TITLE OF INVENTION: METHODS OF IDENTIFYING FUNCTIONAL ANTIBODIES
; FILE REFERENCE: A-890A
; CURRENT APPLICATION NUMBER: US/11/019,027
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: 60/605,902
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: 60/531,714
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: ER localization signal
US-11-019-027-17

Query Match      50.0%; Score 21; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      3 RDDL 6
DB      1 RDDL 4

RESULT 4
US-11-096-706-52
; Sequence 52, Application US/11096706
; Publication No. US20050245476A1

; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; FILE REFERENCE: 019496-008200S
; CURRENT APPLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 60/560,535
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/576,757
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein recognition
; OTHER INFORMATION: region)
US-11-096-706-52

Query Match      50.0%; Score 21; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      3 RDDL 6
DB      2 RDDL 5

RESULT 5
US-11-225-686-208
; Sequence 208, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / 511-US2
; CURRENT APPLICATION NUMBER: US/11/225,686
; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 208
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-11-225-686-208

Query Match      50.0%; Score 21; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches      4; Conservative      1; Mismatches      1; Indels      0; Gaps      0;

QY      3 RDDL 8
DB      1 RSDLLQ 6

RESULT 6
US-11-225-686-211
; Sequence 211, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / 511-US2
; CURRENT APPLICATION NUMBER: US/11/225,686
```

```

; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-11-225-686-211

Query Match          50.0%; Score 21; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 RDDLE 8
        | |||:
Db      1 RSDLLQ 6

RESULT 7
US-11-225-686-216
; Sequence 216, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/225,686
; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 216
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-11-225-686-216

Query Match          50.0%; Score 21; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 RDDLE 8
        | |||:
Db      1 RSDLLQ 6

RESULT 8
US-11-202-009-208
; Sequence 208, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/202,009
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 208
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-11-202-009-208

Query Match          50.0%; Score 21; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 RDDLE 8
        | |||:
Db      1 RSDLLQ 6

RESULT 9
US-11-202-009-211
; Sequence 211, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/202,009
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-11-202-009-211

Query Match          50.0%; Score 21; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 RDDLE 8
        | |||:
Db      1 RSDLLQ 6

RESULT 10
US-11-202-009-216
; Sequence 216, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/202,009
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 216
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-11-202-009-216

Query Match          50.0%; Score 21; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 RDDLE 8
```

Db 1 RSDLLQ 6

```

RESULT 11
US-10-989-767A-219
; Sequence 219, Application US/10989767A
; Publication No. US20060018917A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAF, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALILITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 511582005004
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: 10/277,292
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 219
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide motif
US-10-989-767A-219

```

```

Query Match 50.0%; Score 21; DB 6; Length 9;
Best Local Similarity 37.5%; Pred. No. 1.4e+05;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 VRDLDLE 8
Db 1 LKSDLVE 8

```

```

RESULT 12
US-10-989-767A-565
; Sequence 565, Application US/10989767A
; Publication No. US20060018917A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAF, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALILITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 511582005004
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: 10/277,292
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22

```

```

; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 565
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide motif
US-10-989-767A-565

```

```

Query Match 50.0%; Score 21; DB 6; Length 9;
Best Local Similarity 37.5%; Pred. No. 1.4e+05;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 VRDLDLE 8
Db 1 LKSDLVE 8

```

```

RESULT 13
US-10-989-767A-159
; Sequence 159, Application US/10989767A
; Publication No. US20060018917A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAF, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALILITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 511582005004
; CURRENT APPLICATION NUMBER: US/10/989,767A
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: 10/277,292
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 159
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide motif
US-10-989-767A-159

```

```

Query Match 50.0%; Score 21; DB 6; Length 10;
Best Local Similarity 33.3%; Pred. No. 1.7e+02;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 VRDLDLE 9
Db 1 LINDNAIS 9

```

```

RESULT 14
US-10-989-767A-268
; Sequence 268, Application US/10989767A
; Publication No. US20060018917A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE

```

APPLICANT: RAITANO, ARTHUR
APPLICANT: APAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: CHALLITA-EID, PIA
APPLICANT: JAKOBOVITZ, AVA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
FILE REFERENCE: 511582005004
CURRENT APPLICATION NUMBER: US/10/989,767A
PRIOR FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: 10/277,292
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: 09/935,430
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227,098
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/282,739
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 700
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 268
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chemically synthesized peptide motif
US-10-989-767A-268

Query Match 50.0%; Score 21; DB 6; Length 10;
Best Local Similarity 37.5%; Pred. No. 1.7e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLKDDLE 8
::|||
DB 2 LKMSDLVE 9

RESULT 15
US-10-989-767A-272
Sequence 272, Application US/10989767A
Publication No. US20060018917A1
GENERAL INFORMATION:
APPLICANT: PARIS, MARY
APPLICANT: HUBERT, RENE
APPLICANT: RAITANO, ARTHUR
APPLICANT: APAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: CHALLITA-EID, PIA
APPLICANT: JAKOBOVITZ, AVA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
FILE REFERENCE: 511582005004
CURRENT APPLICATION NUMBER: US/10/989,767A
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: 10/277,292
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: 09/935,430
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227,098
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/282,739
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 700
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 272
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chemically synthesized peptide motif
US-10-989-767A-272

Query Match 50.0%; Score 21; DB 6; Length 10;
Best Local Similarity 37.5%; Pred. No. 1.7e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLKDDLE 8
::|||
DB 1 LKMSDLVE 8

Search completed: April 6, 2006, 17:29:29
Job time : 12.6667 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 6, 2006, 16:12:46 ; Search time 111.667 Seconds
(without alignments)
35.413 Million cell updates/sec

Title: US-10-791-217a-1

Perfect score: 37

Sequence: 1 VLXDDLLEA 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 401289

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	97.3	9	2	AAW99195 Minor his
2	36	97.3	9	2	AAW99196 Minor his
3	36	97.3	9	2	AAW99197 Minor his
4	36	97.3	9	2	AAW97572 T-cell ep
5	36	97.3	9	2	AAW97575 HA-1 H-al
6	36	97.3	9	2	AAW97374 HA-1 R-al
7	36	97.3	9	2	AAW97374 HA-1 R-al
8	36	97.3	9	2	ADH40333 Human min
9	36	97.3	9	2	ADH40334 Human min
10	26	70.3	9	8	ADT73023 Human RSV
11	24	64.9	9	9	ADY01546 SARS coro
12	24	64.9	9	9	ADZ50925 Y. pestis
13	23	62.2	9	5	AAU71211 Human MHC
14	23	62.2	9	5	AAU71428 Human MHC
15	23	62.2	9	8	ADT73690 Human RSV
16	23	62.2	9	8	ADT72767 Human RSV
17	23	62.2	9	9	ADW23047 SARS coro
18	22	59.5	9	3	AAU80162 HLA-A2 re
19	22	59.5	9	5	AAU09449 Chlamydia
20	22	59.5	9	6	ABP75298 Proteome
21	22	59.5	9	6	ABP75138 Proteome
22	22	59.5	9	6	ABP75181 Proteome
23	22	59.5	9	8	ADT72766 Human RSV
24	22	59.5	9	8	ADT73689 Human RSV

25	22	59.5	9	8	ADU99853 BC24 tumor
26	22	59.5	9	8	ABY01301 SARS coro
27	22	59.5	9	9	ADZ57184 Cytotoxic
28	21	56.8	6	3	ABY12035 Peptide #
29	21	56.8	6	5	AAU08010 Rat Rb-in
30	21	56.8	6	7	ADZ84629 Mammalia
31	21	56.8	8	3	AAU12089 Ad7 cel P
32	21	56.8	8	7	ADZ84662 Adenoviru
33	21	56.8	9	2	AAU47427 Prey1 dl
34	21	56.8	9	2	AAU97373 Peptide e
35	21	56.8	9	3	AAU12092 Ad40 cel
36	21	56.8	9	3	AAU12086 Cel motif
37	21	56.8	9	4	ABY12506 Human C35
38	21	56.8	9	4	ABY13927 Human C35
39	21	56.8	9	4	ABY12554 Human C35
40	21	56.8	9	4	ABY13072 Human C35
41	21	56.8	9	4	ABY13115 Human C35
42	21	56.8	9	4	ABY13184 Human C35
43	21	56.8	9	4	ABY13867 Human C35
44	21	56.8	9	4	ABY14131 Human C35
45	21	56.8	9	4	ABY12498 Human C35

ALIGNMENTS

RESULT 1	AAW99195	standard; peptide; 9 AA.
ID	AAW99195	
XX	AAW99195;	
XX	20-MAY-1999	(first entry)
XX	Minor histocompatibility antigen HA-1 T-cell epitope #1.	
XX	Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;	
XX	grat versus host disease; bone marrow transplant; leukaemia; vaccine;	
XX	diagnosis; aplastic anaemia; immune deficiency disease.	
OS	Homo sapiens.	
OS	Synthetic.	
FX	Key	Location/Qualifiers
FT	Misc-difference 3	/label= His, Arg
FT	WT	
XX	MO9905174-A1.	
XX	04-FEB-1999.	
PD	23-JUL-1998;	98WO-NL000425.
XX	23-JUL-1997;	97EP-00202303.
XX	(UTLR-) RIKSUNIV LEIDEN.	
XX	Goulimy EAM, Hunt DF, Engelhard VH;	
XX	WPI, 1999-153312/13.	
XX	A new minor histocompatibility antigen, HA-1 - useful to treat immune	
XX	diseases and prevent rejection and host versus graft disease in bone	
XX	marrow and organ transplantation.	
PS	Claim 1; Page 32; 47pp; English.	
CC	The present sequence represents a new peptide (P1) constituting a T-cell	
CC	epitope obtainable from the minor histocompatibility antigen HA-1. The	
CC	peptide is immunogenic and can be used as part of a vaccine. P1 is used	
CC	as a medicine, to induce tolerance for transplants, prevent rejection	
CC	and/or graft versus host disease, or to treat (auto) immune diseases. In	
CC	particular it can be used with bone marrow transplantation, in the	

```

CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases
XX
SQ Sequence 9 AA;
    Query Match          97.3%; Score 36; DB 2; Length 9;
    Best Local Similarity 100.0%; Pred. No. 2e+06;
    Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLXDDLLEA 9
      |||||
Db      1 VLXDDLLEA 9

RESULT 2
AAW9196 standard; peptide; 9 AA.
XX
AC AAW9196;
XX
DT 20-MAY-1999 (first entry)
XX
DE Minor histocompatibility antigen HA-1 T-cell epitope #2.
XX
KW Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS Homo sapiens.
XX
PN WO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LRIIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-153312/13.
XX
PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
XX
PS Claim 3; Page 32; 47pp; English.
XX
CC The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases
XX
SQ Sequence 9 AA;
    Query Match          97.3%; Score 36; DB 2; Length 9;
    Best Local Similarity 88.9%; Pred. No. 2e+06;
    Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 VLXDDLLEA 9
      |||||
Db      1 VLXDDLLEA 9

RESULT 3
AAW9197 standard; peptide; 9 AA.
ID AAW9197

```

```

XX AAW9197;
AC 20-MAY-1999 (first entry)
XX
DT Minor histocompatibility antigen HA-1 T-cell epitope #3.
XX
DE Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
XX KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
XX KW diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS Homo sapiens.
XX
PN WO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LRIIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-153312/13.
XX
PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
XX
PS Disclosure; Page 15; 47pp; English.
XX
CC The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases
XX
SQ Sequence 9 AA;
    Query Match          97.3%; Score 36; DB 2; Length 9;
    Best Local Similarity 88.9%; Pred. No. 2e+06;
    Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 VLXDDLLEA 9
      |||||
Db      1 VLXDDLLEA 9

RESULT 4
AAW97572 standard; peptide; 9 AA.
ID AAW97572
XX
AC AAW97572;
XX
DT 20-MAY-1999 (first entry)
XX
DE T-cell epitope from the minor histocompatibility antigen HA-1.
XX
KW T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
KW transplant rejection; Graft-versus-Host Disease; autoimmune disease;
KW neoplastic haematopoietic cell.
XX
OS Homo sapiens.
XX
PN Key Location/Qualifiers
XX
FT Misc-difference 3 /note= "His or Arg"
XX

```

PN WO9905173-A1.
 XX 04-FEB-1999;
 XX
 PF 23-JUL-1998; 98WO-NL000424.
 XX
 PR 23-JUL-1997; 97EP-00202303.
 XX
 PA (UYLE-) RIJKSUNIV LEIDEN.
 XX
 PI Goulmy EAJM, Hunt DF, Engelhard VH;
 XX
 DR WPI; 1999-142855/12.
 XX
 PT Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
 PT for inducing tolerance to transplants and prevent rejection or graft-
 PT versus-host disease.
 XX
 PS Claim 1; Page 39; 57pp; English.
 XX
 CC The present sequence represents an immunogenic peptide constituting a T-
 CC cell epitope, obtainable from the minor histocompatibility antigen HA-1.
 CC The peptide can be used in vaccines or pharmaceutical formulations as
 CC medicines to induce tolerance for transplants so as to prevent rejection
 CC and/or Graft-versus-Host Disease, or to treat autoimmune diseases.
 CC Neoplastic haematopoietic cells presenting the peptides, in an HLA class
 CC I context, can be eliminated after specific recognition of the peptides.
 CC The peptides can also be used to raise antibodies, T-cell receptor, B-
 CC and T-cells.
 XX
 SQ Sequence 9 AA;

Query Match 97.3%; Score 36; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
 |||||
 1 VLXDDLLEA 9

Db

RESULT 5
 AAM97375
 ID AAM97375 standard; protein; 9 AA.
 XX
 AC AAM97375;
 XX
 DT 13-MAY-1999, (first entry)
 XX
 DE HA-1 H-allele sequence.
 XX
 KM Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
 KM R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
 KM severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO9905313-A2.
 XX
 PD 04-FEB-1999.
 XX
 PF 23-JUL-1998; 98WO-EP004928.
 XX
 PR 23-JUL-1997; 97EP-00202303.
 PR 02-JUN-1998; 98EP-00870125.
 XX
 PA (UYLE-) RIJKSUNIV LEIDEN.
 XX
 PI Goulmy E;
 XX
 DR WPI; 1999-142960/12.
 XX
 PT Typing minor histocompatibility antigen HA-1 - by amplifying and

PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
 PT of genetic aberrances.
 XX
 PS Claim 18; Fig 5; 59pp; English.
 XX
 CC The present sequence represents part of the minor histocompatibility
 CC antigen HA-1 H-allele. The specification describes methods for typing
 CC alleles (preferably the H and R alleles) of the minor histocompatibility
 CC antigen HA-1 in a sample, which comprise detecting polymorphic
 CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
 CC methods can be used for HA-1 typing for bone marrow transplants, severe
 CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
 CC detection of genetic aberrances. The probes and primers of the invention
 CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
 CC anti-idiotypic B cells and/or T cells and antibodies
 XX
 SQ Sequence 9 AA;

Query Match 97.3%; Score 36; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
 |||||
 1 VLXDDLLEA 9

Db

RESULT 6
 AAM97374
 ID AAM97374 standard; protein; 9 AA.
 XX
 AC AAM97374;
 XX
 DT 13-MAY-1999 (first entry)
 XX
 DE HA-1 R-allele sequence.
 XX

KM Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
 KM R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
 KM severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO9905313-A2.
 XX
 PD 04-FEB-1999.
 XX
 PF 23-JUL-1998; 98WO-EP004928.
 XX
 PR 23-JUL-1997; 97EP-00202303.
 PR 02-JUN-1998; 98EP-00870125.
 XX
 PA (UYLE-) RIJKSUNIV LEIDEN.
 XX
 PI Goulmy E;
 XX
 DR WPI; 1999-142960/12.
 XX
 PT Typing minor histocompatibility antigen HA-1 - by amplifying and
 PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
 PT of genetic aberrances.
 XX
 PS Claim 13; Fig 5; 59pp; English.
 XX
 CC The present sequence represents part of the minor histocompatibility
 CC antigen HA-1 R-allele. The specification describes methods for typing
 CC alleles (preferably the H and R alleles) of the minor histocompatibility
 CC antigen HA-1 in a sample, which comprise detecting polymorphic
 CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
 CC methods can be used for HA-1 typing for bone marrow transplants, severe
 CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
 CC detection of genetic aberrances. The probes and primers of the invention
 CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used

CC anti-idiotypic B cells and/or T cells and antibodies
XX Sequence 9 AA;
SQ

Query Match 97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLEA 9
|||
1 VLXDDLEA 9

RESULT 7
ADH40333
ID ADH40333 standard; peptide; 9 AA.

XX AC ADH40333;

XX DT 11-MAR-2004 (first entry)

XX DE Human minor histocompatibility antigen HA-1 T cell epitope.

XX human, cytostatic; vaccine; SNP profile; cancer; leukaemia;

XX minor histocompatibility antigen; mHag; T cell epitope.

XX OS Homo sapiens.

XX PA WO2003106692-A2.

XX PN 24-DEC-2003.

XX PD 13-JUN-2003; 2003WO-EP006251.

XX PF 13-JUN-2002; 2002EP-00013423.

XX PR (MERE) MERCK PATENT GMBH.

XX PA Stittmattner W, Moll H;

XX PI WPI; 2004-082200/08.

XX PT Providing allelic variant epitope of protein based on single nucleotide
XX polymorphism by defining target protein, screening database of protein,
XX identifying, selecting allelic variant protein, creating variant
XX epitopes.

XX PS Disclosure; Page 82; 119pp; English.

XX The invention relates to a novel method for providing epitopes of allelic
XX variants of antigenic proteins from specific species based on single
XX nucleotide polymorphism (SNP), by defining target protein/peptide or its
XX subsect, screening database of DNA encoding target protein, identifying,
XX selecting allelic peptide/protein variants, expression product or its
XX fragment encoded by DNA sequence having SNP, creating variant epitopes,
XX CC selecting epitopes binding to MHC protein. A protein of the invention has
XX cytostatic activity, and may have a use in a vaccine. The method is
XX useful for generating a SNP profile of one or more individuals from a
XX given species by applying the method for several protein from the
XX individuals, where the SNP profile was related to disease, preferably
XX cancer. This is useful for diagnosing a disease in an individual by
XX generating the SNP-related polymorphic profile. A method of the invention
XX is useful for transplanting haematopoietic stem cells from a donor to a
XX recipient and treating cancer, preferably leukaemia, and for determining
XX the progression, regression or onset of a treated disease. The present
XX sequence is used in the exemplification of the invention.

XX SQ Sequence 9 AA;

Query Match 97.3%; Score 36; DB 8; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLEA 9
|||
1 VLXDDLEA 9

RESULT 8
ADH40334
ID ADH40334 standard; peptide; 9 AA.

XX AC ADH40334;

XX DT 11-MAR-2004 (first entry)

XX DE Human minor histocompatibility antigen HA-1 T cell epitope.

XX human, cytostatic; vaccine; SNP profile; cancer; leukaemia;

XX minor histocompatibility antigen; mHag; T cell epitope.

XX OS Homo sapiens.

XX PA WO2003106692-A2.

XX PN 24-DEC-2003.

XX PD 13-JUN-2003; 2003WO-EP006251.

XX PF 13-JUN-2002; 2002EP-00013423.

XX PR (MERE) MERCK PATENT GMBH.

XX PA Stittmattner W, Moll H;

XX PI WPI; 2004-082200/08.

XX PT Providing allelic variant epitope of protein based on single nucleotide
XX polymorphism by defining target protein, screening database of protein,
XX identifying, selecting allelic variant protein, creating variant
XX epitopes.

XX PS Disclosure; Page 82; 119pp; English.

XX The invention relates to a novel method for providing epitopes of allelic
XX variants of antigenic proteins from specific species based on single
XX nucleotide polymorphism (SNP), by defining target protein/peptide or its
XX subsect, screening database of DNA encoding target protein, identifying,
XX selecting allelic peptide/protein variants, expression product or its
XX fragment encoded by DNA sequence having SNP, creating variant epitopes,
XX CC selecting epitopes binding to MHC protein. A protein of the invention has
XX cytostatic activity, and may have a use in a vaccine. The method is
XX useful for generating a SNP profile of one or more individuals from a
XX given species by applying the method for several protein from the
XX individuals, where the SNP profile was related to disease, preferably
XX cancer. This is useful for diagnosing a disease in an individual by
XX generating the SNP-related polymorphic profile. A method of the invention
XX is useful for transplanting haematopoietic stem cells from a donor to a
XX recipient and treating cancer, preferably leukaemia, and for determining
XX the progression, regression or onset of a treated disease. The present
XX sequence is used in the exemplification of the invention.

XX SQ Sequence 9 AA;

Query Match 97.3%; Score 36; DB 8; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLEA 9
|||
1 VLXDDLEA 9

RESULT 9
ADT73023
ID ADT73023 standard; peptide; 9 AA.

XX ADT73023;
XX 13-JAN-2005 (first entry)
XX Human RSV L high affinity binding peptide Segid 919.
XX human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
XX MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.
XX Human respiratory syncytial virus.
XX WO2004092207-A2.
XX 28-OCT-2004.
XX 16-APR-2004; 2004WO-EP004061.
XX 16-APR-2003; 2003BP-00447095.
XX (ALGO-) ALGONOMICS NV.
XX Laesters I, Desmet J, Stegmann T;
XX WPI; 2004-758334/74.
XX New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
XX or P) for inducing an immune response to RSV or for diagnosing,
XX preventing or treating viral infections, particularly RSV infection.
XX Claim 16; SEQ ID NO 919; 143BP; English.
XX This invention relates to novel isolated or purified peptides of the
XX human respiratory syncytial virus (RSV), in particular ten RSV genes
XX encoding 11 separate viral proteins: non-structural proteins NS-1 (also
XX known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and
XX eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
XX SH (also known as the 1A protein). Specifically, it refers to a
XX composition comprising an above peptide mixed with a pharmaceutical
XX excipient or an RSV immunogenic composition comprising a recombinant
XX expression vector with a nucleic acid insert encoding an above peptide.
XX The present invention describes an in vitro method of detecting cytotoxic
XX T lymphocytes (CTLs) that respond to a major histocompatibility complex
XX (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
XX RSV peptide is useful for preparing a diagnostic composition or an RSV
XX immunisation, or for preparing an immune response provoking vaccine in
XX the event of RSV infection (the vaccine being prepared by contacting the
XX polypeptide in an immune response-provoking amount of specific CTL).
XX Accordingly, these peptide compositions have virucidal activity. This
XX peptide sequence is a human RSV high binding affinity peptide of the
XX invention.
XX Sequence 9 AA;
SQ

Query Match 70.3%; Score 26; DB 8; Length 9;
Best Local Similarity 44.4%; Pred. No. 2e+06;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLXDDLLLA 9
DB 1 IIXDDILSA 9

RESULT 10
ID ABY01546 standard; peptide; 9 AA.
XX ABY01546;
XX ABY01546;
XX 16-JUN-2005 (first entry)
XX SARS coronavirus spike protein HLA A 0201 T-cell epitope, SEQ:8174.
DE

XX Vaccine; nucleic acid vaccine; drug screening; diagnosis;
XX SARS coronavirus infection; infection; respiratory disease; virucide.
XX SARS coronavirus.
XX WO2004092360-A2.
XX 26-OCT-2004.
XX 09-APR-2004; 2004WO-US011710.
XX 10-APR-2003; 2003US-0462218P.
XX 11-APR-2003; 2003US-0462465P.
XX 12-APR-2003; 2003US-0462418P.
XX 13-APR-2003; 2003US-0462748P.
XX 14-APR-2003; 2003US-0463109P.
XX 15-APR-2003; 2003US-0463460P.
XX 16-APR-2003; 2003US-0463668P.
XX 17-APR-2003; 2003US-0463983P.
XX 18-APR-2003; 2003US-0463971P.
XX 22-APR-2003; 2003US-0464838P.
XX 22-APR-2003; 2003US-0464899P.
XX 23-APR-2003; 2003US-0465273P.
XX 24-APR-2003; 2003US-0465353P.
XX 05-MAY-2003; 2003US-0468312P.
XX 22-MAY-2003; 2003US-0473144P.
XX 14-JUG-2003; 2003US-0495024P.
XX 23-SEP-2003; 2003US-0505652P.
XX 11-OCT-2003; 2003US-0510781P.
XX 11-DEC-2003; 2003US-0529464P.
XX 12-JAN-2004; 2004US-0536177P.
XX 07-APR-2004; 2004US-0560757P.
XX (CHIR) CHIRON CORP.
XX Rappoli R, Masignani V, Stadler K, Gregersen J, Chien D, Han J,
XX Polo J, Weiner A, Houghton M, Song HC, Seo MY, Donnelly JF,
XX Kleink HD, Valiante N;
XX WPI; 2004-766863/75.
XX Novel isolated polypeptide e.g. spike polypeptide, Env polypeptide, of
XX severe acute respiratory syndrome virus (SARS), useful as vaccine for
XX SARS.
XX Disclosure; SEQ ID NO 8174; 839BP; English.
XX The invention relates to isolated polypeptides of the severe acute
XX respiratory syndrome (SARS) coronavirus. The polypeptides include spike
XX (S or E2), env (E or 8M), membrane (M or E1), hemagglutinin-esterase (HS
XX or E3), and nucleocapsid (N) polypeptides, and the ORF1a and ORF1ab
XX (replicase) polypeptides and their proteolytic fragments. The invention
XX also relates to antibodies which recognise the polypeptides; nucleic
XX acids encoding the SARS virus polypeptides; primers specific for SARS
XX virus nucleic acid sequences; kits for amplifying SARS virus target
XX nucleic acids; a double-stranded RNA molecule 10-30 nucleotides in length
XX which is able to inactivate the SARS virus in a mammalian cell; an
XX expression construct for recombinant expression of a SARS virus spike
XX protein; a viral vector for in vivo delivery of a SARS virus polypeptide-
XX encoding nucleic acid; and a mammalian cell line stably expressing a SARS
XX viral antigen. The invention additionally provides a vaccine for the
XX treatment or prevention of SARS comprising an inactivated SARS virus, a
XX killed SARS virus, an attenuated SARS virus, a split SARS virus
XX preparation, or at least one purified SARS virus antigens; methods of
XX making inactivated SARS virus and vaccines containing it; an alpha-virus
XX replicon particle comprising one or more SARS viral antigens; and a
XX vaccine comprising one or more SARS virus antigens and one or more
XX respiratory virus antigens. The invention further encompasses a method of
XX identifying a therapeutically active agent by measuring the effect of the
XX agent on a SARS-related enzyme, and a method of treating a SARS patient
XX using small molecule viral inhibitors. The SARS virus polypeptides and
XX nucleic acids can be used in the preparation and manufacture of vaccines

CC for the treatment or prevention of SARS. The SARS virus polypeptides,
CC antibodies against them, and SARS virus-specific primers and kits
CC containing them are useful for diagnosing or identifying the presence of
CC SARS in a biological sample. The present sequence represents a SARS
CC coronavirus T-cell epitope. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 9 AA:

CC for inducing immune response in a subject (said immunity to Yersinia
CC pestis infection, the causative agent of plague). The present sequence is
CC a cytotoxic Yersinia pestis T-cell epitope of the invention.
XX
SQ Sequence 9 AA:

Query Match. 64.9%; Score 24; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0

Query Match	64.9%	Score 24	DB 8	Length 9
Best Local Similarity	44.4%	Pred. No. 2e+06		
Matches 4; Conservative		3; Mismatches	2; Indels	0; Gaps

Query Match	64.9%	Score 24	DB 9	Length 9	
Best Local Similarity	62.5%	Pred. No. 2e+06			
Matches	5	Conservative	1	Mismatches	2
				Indels	0
				Gaps	0
QY	1	VIXDDILE	8		
		:			
DB	1	LHDDALE	8		

```
QY      1 VLXDDLLEA 9
        :| | | :|
Db      1 LITDDMIAA 9
```

```

RESULT 12
AAU71211
ID      AAU71211 standard; peptide; 9 AA.

```

RESULT 11
ADZ50925
ID ADZ50925 standard; peptide; 9 AA.

DT 26-FEB-2002 (first entry)
XX

AC ADZ50925;

XX

DT 14-JUL-2005 (first entry)

KW tumour; cancer; cytostatic; gene therapy; antibody therapy; ribozyme;

DE Y. pestis cytotoxic T-cell epitope SEQ ID 993.

KW chromosome 9q13-q21.

Yersinia pestis infection; antibacterial; infection; epitope; T-cell; vaccine; biological warfare.

OS Homo sapiens.
XX

Yersinia pestis.

XX

PN WO2005037855-A2.

2000

PD 28-APR-2005.

XX

PF 15-OCT-2004; 2004WO-US033883.

XX
RECORD TWO

PR 17-OCT-2003; 2003US-0511653P

XX
XX

PA (PECO-) PECOS LABS INC.

PI Jakobovits A;

PI Lund O, Lundegaard C, Nielsen M, Worning P, Deans RJ, Buus S;

DR WPI; 2002-061976/08.

XX

PT Monitoring 103P3E8 gene products in sample from patient (suspected of)

PT New cytotoxic *Yersinia pestis* T-cell epitope comprising 10 amino acids, PT useful as a vaccine or diagnostic tool and for inducing immune response in a subject.

PT products.
XX
PS Disclosure; Page 84; 128pp; English.

PS Claim 1; SEQ ID NO 993; 235pp; English

CC Sequences AAU71093-AAU71796 represented

The invention relates to a cytotoxic *Yersinia pestis* T-cell epitope, selected from any of the 1000 sequences of 9 amino acids appearing as ADZ49933-ADZ50932. Also included are predicting peptides that are epitopes or can be used as diagnostic tools (comprising predicting which peptides bind to a HMC molecule (not defined) with high affinity using a neural network with at least one of the following features: some or all of the inputs to the neural networks are generated using a hidden Markov model; or some or all of the inputs are encoded by an amino acid substitution matrix, different from an identity matrix) and a vaccine or diagnostic tool using a limited number such as at least 1, 2, 3, 4, 5, 8, 16, 32, 64, 128, 256, 512 of the peptides of ADZ49933-ADZ50933. In predicting peptides, the prediction of the neural network is combined with prediction or measurement of one of the following: professional cleavage sites; MHC binding; presence of sequence or related sequence(s) in patent databases; TAP binding; gene or protein expression level; function of the protein; localisation of the protein; and similarly to self proteins. The epitope is useful as a vaccine or diagnostic tool, and

AA Sequences AAU71093-AAU71796 represent the 103P38-related protein and peptide fragments of the protein. 103P38 exhibits tissue specific CC expression in normal adult tissue, but it is also aberrantly expressed in CC many cancers including tumors of the prostate, bladder, kidney, colon, CC lung, breast, rectum and stomach. The 103P38 polynucleotide, its related CC protein and peptide fragments and specific PCR primers are therefore CC useful for diagnosing and treating cancer. A vector comprising a CC polynucleotide which encodes a single chain monoclonal antibody, that CC immunospecifically binds to an 103P38-related protein, and a ribozyme CC capable of cleaving a polynucleotide having the 103P38 coding sequence, CC are both useful in the preparation of a composition for treating a CC patient with a cancer that expresses 103P38. The sequences can be used CC in diagnostic methods to monitor the level of 103P38 gene products in CC serum, blood, urine and tissue and to thereby detect the presence of CC cancerous cells

XX
CC
SQ Sequence 9 AA;

Query Match 62.2%; Score 23; DB 5; Length 9;

Query Match 62.2%; Score 23; DB 5; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DILEA 9
|||||
DB 1 DILEA 5

RESULT 13

AAU71428
ID AAU71428 standard; peptide; 9 AA.

XX AAU71428;
XX

DT 26-FEB-2002 (first entry)
XX

DE Human MHC molecule HLA-A11 binding 103P3B8 peptide #35.
XX

XX 103P3B8; prostate; bladder; kidney; colon; lung; breast; rectum; stomach;
KW tumour; cancer; cytostatic; gene therapy; antibody therapy; ribozyme;
KW single chain monoclonal antibody; serum; blood; urine; tissue; human;
KW chromosome 9q13-q21.

XX Homo sapiens.
OS

XX WO200179557-A2.
PN

XX 25-OCT-2001.
PD

XX 12-APR-2001; 2001WO-US012181.
PF

XX 12-APR-2000; 2000US-0196647P.
PR

XX (UROG-) UROGENESYS INC.
PA

XX Faris M, Challita-Eid PM, Raitano AB, Mitchell SC, Afar DEH;
PI Jakobovits A;
PI

XX WPI; 2002-061976/08.
DR

XX Monitoring 103P3B8 gene products in sample from patient (suspected of)
PT having cancer, useful for diagnosing, managing or treating cancers, e.g.
PT prostate cancer, comprises determining presence of aberrant 103P3B8 gene
PT products.

XX Disclosure; Page 90; 128pp; English.
PS

XX Sequences AAU71093-AAU71796 represent the 103P3B8-related protein and
CC peptide fragments of the protein. 103P3B8 exhibits tissue specific
CC expression in normal adult tissue, but it is also aberrantly expressed in
CC many cancers including tumours of the prostate, bladder, kidney, colon,
CC lung, breast, rectum and stomach. The 103P3B8 polynucleotide, its related
CC protein and peptide fragments and specific PCR primers are therefore
CC useful for diagnosing and treating cancer. A vector comprising a
CC polynucleotide which encodes a single chain monoclonal antibody, that
CC immunospecifically binds to an 103P3B8-related protein, and a ribozyme,
CC capable of cleaving a polynucleotide having the 103P3B8 coding sequence,
CC are both useful in the preparation of a composition for treating a
CC patient with a cancer that expresses 103P3B8. The sequences can be used
CC in diagnostic methods to monitor the level of 103P3B8 gene products in
CC serum, blood, urine and tissue and to thereby detect the presence of
CC cancerous cells
CC

XX Sequence 9 AA;
SQ

Query Match 62.2%; Score 23; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DILEA 9
|||||
DB 5 DILEA 9

RESULT 14

ADT73690
ID ADT73690 standard; peptide; 9 AA.

XX ADT73690;
XX

DT 13-JAN-2005 (first entry)
XX

DE Human RSV L high affinity binding peptide SegID 1586.
XX

XX human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
KW MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.
XX

OS Human respiratory syncytial virus.
XX

XX WO2004092207-A2.
PN

XX 28-OCT-2004.
PD

XX 16-APR-2004; 2004WO-EP004061.
PF

XX 16-APR-2003; 2003EP-00447095.
PR

XX (ALGO-) ALGONOMICS NV.
PA

XX Lasters I, Desmet J, Stegmann T;
PI

XX WPI; 2004-758334/74.
DR

XX New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
PT or P) for inducing an immune response to RSV or for diagnosing,
PT preventing or treating viral infections, particularly RSV infection.

XX Claim 16; SEQ ID NO 1586; 143pp; English.
PS

XX This invention relates to novel isolated or purified peptides of the
CC human respiratory syncytial virus (RSV), in particular ten RSV genes
CC encoding 11 separate viral proteins: non-structural proteins NS-1 (also
CC known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and
CC eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
CC SH (also known as the 1A protein). Specifically, it refers to a
CC composition comprising an above peptide mixed with a pharmaceutical
CC excipient or an RSV immunogenic composition comprising a recombinant
CC expression vector with a nucleic acid insert encoding an above peptide.
CC The present invention describes an in vitro method of detecting cytotoxic
CC T lymphocytes (CTLs) that respond to a major histocompatibility complex
CC (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
CC RSV peptide is useful for preparing a diagnostic composition or an RSV
CC (prophylactic or therapeutic) vaccine composition for a DNA-based
CC immunisation, or for preparing an immune response provoking vaccine in
CC the event of RSV infection (the vaccine being prepared by contacting the
CC polypeptide in an immune response-provoking amount of specific CTL).
CC Accordingly, these peptide compositions have virucidal activity. This
CC peptide sequence is a human RSV high binding affinity peptide of the
CC invention.
CC

XX Sequence 9 AA;
SQ

Query Match 62.2%; Score 23; DB 8; Length 9;
Best Local Similarity 44.4%; Pred. No. 2e+06;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLKDDLEA 9
::||:|
DB 1 IIKDDILA 9

RESULT 15

ADT72767
ID ADT72767 standard; peptide; 9 AA.

XX ADT72767;
AC

XX 13-JAN-2005 (first entry)
 DT Human RSV L high affinity binding peptide SegID 663.
 DE human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
 KW MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.
 XX Human respiratory syncytial virus.
 OS WO2004092207-A2.
 PN 28-OCT-2004.
 PD 16-APR-2004; 2004WO-EP004061.
 XX 16-APR-2003; 2003EP-00447095.
 PR (ALGO-) ALGONOMICS NV.
 XX (ALGO-) ALGONOMICS NV.
 PA Lasters I, Desmet J, Stegmann T;
 PI WPI; 2004-758334/74.
 DR New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
 XX or P) for inducing an immune response to RSV or for diagnosing,
 PT preventing or treating viral infections, particularly RSV infection.
 XX Disclosure; SEQ ID NO 663; 143bp; English.
 PS
 XX
 CC This invention relates to novel isolated or purified peptides of the
 CC human respiratory syncytial virus (RSV), in particular ten RSV genes
 CC encoding its separate viral proteins: non-structural proteins NS-1 (also
 CC known as the IC protein) & NS-2 (IB protein), a polymerase protein L and
 CC eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
 CC SH (also known as the 1A protein). Specifically, it refers to a
 CC composition comprising an above peptide mixed with a pharmaceutical
 CC excipient or an RSV immunogenic composition comprising a recombinant
 CC expression vector with a nucleic acid insert encoding an above peptide.
 CC The present invention describes an in vitro method of detecting cytotoxic
 CC T lymphocytes (CTLs) that respond to a major histocompatibility complex
 CC (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
 CC RSV peptide is useful for preparing a diagnostic composition or an RSV
 CC (prophylactic or therapeutic) vaccine composition for a DNA-based
 CC immunisation, or for preparing an immune response provoking vaccine in
 CC the event of RSV infection (the vaccine being prepared by contacting the
 CC polypeptide in an immune response-provoking amount of specific CTL).
 CC Accordingly, these peptide compositions have virucidal activity. This
 CC peptide sequence is a human RSV high binding affinity peptide of the
 CC invention.
 XX
 SQ Sequence 9 AA;

Query Match 62.2%; Score 23; DB 8; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2e+06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 LKDDLLIA 9
 : ||: ||
 Db 1 IKDDILSA 8

Search completed: April 6, 2006, 16:19:09
 Job time : 113.667 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 6, 2006, 16:19:36 ; Search time 18.6667 Seconds
(without alignments)
46.390 Million cell updates/sec

Title: US-10-791-217A-1

Perfect score: 37

Sequence: 1 VLXDDLRA 9

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	43.2	7	2	S68004
2	16	43.2	8	2	PC4131
3	14	37.8	7	2	S20446
4	13	37.8	7	2	A59489
5	13	35.1	8	2	A61328
6	13	35.1	9	2	PH0942
7	13	35.1	9	2	A60427
8	12	32.4	4	2	I40697
9	12	32.4	5	2	PT0679
10	12	32.4	5	2	PT0601
11	12	32.4	6	2	B35640
12	12	32.4	6	2	PT0533
13	12	32.4	7	2	A34026
14	12	32.4	7	2	B39040
15	12	32.4	7	2	PT0628
16	12	32.4	7	2	PT0722
17	12	32.4	7	2	PT0576
18	12	32.4	8	2	PT0557
19	12	32.4	9	2	PH0108
20	12	32.4	9	2	PT0562
21	12	32.4	9	2	B30572
22	12	32.4	9	2	PS0253
23	11	29.7	6	2	T11779
24	11	29.7	7	2	S25266
25	11	29.7	8	2	S24248
26	11	29.7	8	2	B33099
27	11	29.7	8	2	S69165
28	11	29.7	9	2	S66419
29	11	29.7	9	2	PM0002

30	11	29.7	9	2	A12872	transaldolase (EC
31	11	29.7	9	2	A61386	macrophage inhibit
32	10	27.0	4	2	A48360	gamma subunit of p
33	10	27.0	4	2	A26209	protein-glutamine
34	10	27.0	6	2	H48394	glycoprotein compo
35	10	27.0	6	2	I48126	alpha-tubulin - Ch
36	10	27.0	7	2	S78024	ribosomal protein
37	10	27.0	7	2	A12016	formylglycinamide
38	10	27.0	7	2	C56793	platelet glycoprot
39	10	27.0	7	2	S28735	polyposphate-gluc
40	10	27.0	7	2	PC2370	probable H+-transp
41	10	27.0	7	2	T09512	NADH2 dehydrogenas
42	10	27.0	8	2	A32523	peptidyl-dipectida
43	10	27.0	8	2	T10077	hypothetical prote
44	10	27.0	8	2	PT0298	Ig heavy chain CRD
45	10	27.0	8	2	A42057	fibroblast growth

ALIGNMENTS

RESULT 1
S68004
hucolin, 75K chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C/Accession: S68004
R/Idgar, P.F.
FEBS Lett. 375, 159-161, 1995
A/Title: Hucolin, a new corticosteroid-binding protein from human plasma with structural
A/Reference number: S68004; MUID:96087107; PMID:7498469
A/Accession: S68004
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-7 <EDG>
A/Cross-references: UNIPARC:UPI000017C164

Query Match 43.2% Score 16; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDL 6
Db 4 DDL 6

RESULT 2
PC4131
hypothetical protein 8 [imported] - Pseudomonas aeruginosa (fragment)
C/Species: Pseudomonas aeruginosa
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004
C/Accession: PC4131
R/Kawasaki, S.; Arai, H.; Igatahshi, Y.; Kodama, T.
Gene 167, 87-91, 1995

A/Title: Sequencing and characterization of the downstream region of the genes encoding
Y for biosynthesis of heme d1.
A/Reference number: UC4552; MUID:96144254; PMID:8566817
A/Accession: PC4131
A/Status: preliminary
A/Molecule type: DNA

A/Residues: 1-8 <KAW>
A/Cross-references: UNIPROT:P95412; UNIPARC:UPI000017A96A; DDBJ:D50473; NID:G1217594
A/Note: This ORF is not annotated in Genbank entry F5ENIRC, release 113.0
C/Superfamily: Pseudomonas stutzeri n1rd protein

Query Match 43.2% Score 16; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDL 6
Db 2 DDL 4

```
RESULT 3
S20446      elactase - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
C:Accession: S20446
R:Kessler, E.; Safiri, M.; Peretz, M.; Birstein, Y.
FEBS Lett. 293, 291-293, 1992
A:Title: Identification of cleavage sites involved in proteolytic processing of Pseudom
A:Reference number: S20446; MUID:92183956; PMID:1544509
A:Accession: S20446
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <RCS>
A:Cross-references: UNIPARC:UPI000017A95F

Query Match      37.8%; Score 14; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      5 LLE 8
      |||
Db      3 DLD 6

RESULT 4
A59489      protein kinase C inhibitor - rat (fragment)
C:Species: Rattus norvegicus
C:Date: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 25-Aug-2003
C:Accession: A59489
R:Negoro, M.
submitted to the Protein Sequence Database, June 2003
A:Description: Purification of PKC1 from rat liver.
A:Reference number: A59489
A:Accession: A59489
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <NEG>
A:Experimental source: strain Wistar, liver
A:Note: p-Hydroxyacetophenone-Sepharose binding protein

Query Match      37.8%; Score 14; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 VLXD 5
      |||
Db      2 IFED 6

RESULT 5
A61328      trypsin (EC 3.4.21.4) precursor - minke whale (fragment)
C:Species: Balaeoptera acutrostrata (minke whale, lesser rorqual)
C:Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 03-Jul-2004
C:Accession: A61328
R:Bricleux-Gregoire, S.; Schyns, R.; Flojkin, M.; Emmeus, M.; Welling, G.W.; Beintema, J
Biochim. Biophys. Acta 386, 244-255, 1975
A:Title: N-terminal amino acid sequence of trypsinogen from the lesser rorqual, Balaeopt
creat.
A:Reference number: A61328; MUID:75146765; PMID:1125273
A:Accession: A61328
A:Molecule type: protein
A:Residues: 1-8 <BR>
A:Cross-references: UNIPROT:Q7M390; UNIPARC:UPI000017C43P
C:Keywords: hydrolase; protein digestion; serine proteinase; zymogen
F:1-8/Domain: activation peptide #status experimental <APT>

Query Match      35.1%; Score 13; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 LKXD 5
      |||
Db      3 IDDD 6

RESULT 6
PH0942      T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0942
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi
A:Reference number: PH0941; MUID:92078857; PMID:1836012
A:Accession: PH0942
A:Molecule type: mRNA
A:Residues: 1-9 <GOL>
A:Cross-references: UNIPARC:UPI000017C9DD
A:Experimental source: complete Freund's adjuvant-immunized lymph node
A:Note: the authors translated the codon TGC for residue 2 as Ala
C:Keywords: T-cell receptor

Query Match      35.1%; Score 13; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 LLE 8
      |||
Db      5 LLE 7

RESULT 7
A60427      macrophage cytotoxicity-inducing factor, 29K - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: A60427
R:Jones, C.W.; Prince, C.A.; Williams, J.S.
Exp. Hematol. 19, 704-709, 1991
A:Title: Purification and amino acid analysis of a human macrophage cytotoxicity-inducin
A:Reference number: A60427; MUID:91372335; PMID:1909970
A:Accession: A60427
A:Molecule type: protein
A:Residues: 1-9 <JON>
A:Cross-references: UNIPROT:Q7M4R5; UNIPARC:UPI0000142BE0
A:Note: the sequence from the text on page 706 is inconsistent with that from page 708 i
C:Keywords: cytokine

Query Match      35.1%; Score 13; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 VLXD 4
      |||
Db      4 VLXD 7

RESULT 8
I40697      biotin A - Citrobacter freundii (fragment)
C:Species: Citrobacter freundii
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40697
R:Shuan, D.; Campbell, A.
Gene 67, 203-211, 1988
A:Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacte
A:Reference number: I40697; MUID:89006280; PMID:2971595
A:Accession: I40697
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RCS>
```

A:Cross-references: UNIPROT:P13071; UNIPARC:UPI000017NA21; GB:M21922; NID:g144434

Query Match 32.4%; Score 12; DB 2; Length 4;

Best Local Similarity 100.0%; Pred.No.2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 5
||
3 DD 4

RESULT 9

PT0679

T-cell receptor beta chain V-D-J region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0679; PT0708

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; PMID:9127601; PMID:111558

A:Accession: PT0679

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-5 <FE2>

A:Cross-references: UNIPARC:UPI000017C8AD

A:Experimental source: day 18 fetal thymus, strain BALB/c, 154-2J

A:Accession: PT0708

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-5 <FE2>

A:Cross-references: UNIPARC:UPI000017C8AD

A:Experimental source: newborn thymus, strain BALB/c, 161-2B

C:Keywords: T-cell receptor

Query Match 32.4%; Score 12; DB 2; Length 5;

Best Local Similarity 100.0%; Pred.No.2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 5
||
4 DD 5

RESULT 10

PT0601

T-cell receptor beta chain V-D-J region (120-2K) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004

C:Accession: PT0601; PT0617; PT0694

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; PMID:9127601; PMID:111558

A:Accession: PT0601

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-5 <FE3>

A:Cross-references: UNIPROT:Q64512; UNIPARC:UPI000017C7B6

A:Experimental source: newborn thymus, strain BALB/c, 120-2CA

A:Accession: PT0694

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-5 <FE2>

A:Cross-references: UNIPARC:UPI000017C7B6

A:Experimental source: day 18 fetal thymus, strain BALB/c, 154-1H

C:Keywords: T-cell receptor

Query Match 32.4%; Score 12; DB 2; Length 5;

Best Local Similarity 100.0%; Pred.No.2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 5
||
4 DD 5

RESULT 11

B35640

cerebellar degeneration-related protein - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 24-Jun-1993

C:Accession: B35640

R:Chen, Y.T.; Reftig, W.J.; Yenamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, J.

Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990

A:Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal ma

A:Reference number: A35640; PMID:90222173; PMID:2326268

A:Accession: B35640

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-6 <CHE>

A:Cross-references: UNIPARC:UPI000017C63A

Query Match 32.4%; Score 12; DB 2; Length 6;

Best Local Similarity 66.7%; Pred.No.2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 6
||
3 DD 5

RESULT 12

PT0533

T-cell receptor beta chain V-D-J region (126-1AA) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0533

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; PMID:9127601; PMID:111558

A:Accession: PT0533

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-6 <FE2>

A:Cross-references: UNIPARC:UPI000017C801

A:Experimental source: adult thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 32.4%; Score 12; DB 2; Length 6;

Best Local Similarity 100.0%; Pred.No.2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 5
||
4 DD 5

RESULT 13

A34026

acetylcholinesterase (EC 3.1.1.7) 5.6S form - Pacific electric ray (fragment)

C:Species: Torpedo californica (Pacific electric ray)

C>Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 08-Nov-1996

C:Accession: A34026

R:Gibney, G.; MacPhee-Quigley, K.; Thompson, B.; Vedvick, T.; Low, M.G.; Taylor, S.S.;

J. Biol. Chem. 263, 1140-1145, 1988

A:Title: Divergence in primary structure between the molecular forms of acetylcholinest

A:Reference number: A34026; PMID:88087239; PMID:3335534

A:Accession: A34026

A:Molecule type: protein

A:Residues: 1-7 <GIB>

A:Cross-references: UNIPARC:UPI000017BF32

C:Keywords: alternative splicing; carboxylic ester hydrolase

Query Match 32.4%; Score 12; DB 2; Length 7;

Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 LIEA 9

Db 1 ILNA 4

RESULT 14

B39040

calsequestrin, fast skeletal muscle - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997

C:Accession: B39040

R:Calla, S.B.; Jones, L.R.

J. Biol. Chem. 266, 391-398, 1991

A:Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein

A:Reference number: A39040; KWID:91093153; PMID:1985907

A:Accession: B39040

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <CAL>

A:Cross-references: UNIPARC:UPI000017CSBC

C:Keywords: phosphoprotein; skeletal muscle

Query Match 32.4%; Score 12; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DD 5

Db 1 DD 2

RESULT 15

PT0628

T-cell receptor beta chain V-D-J region (111-1AG) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0628

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; KWID:91277601; PMID:1711558

A:Accession: PT0628

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-7 <FEB>

A:Cross-references: UNIPARC:UPI000017C7CD

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 32.4%; Score 12; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DD 5

Db 4 DD 5

Search completed: April 6, 2006, 16:26:10
Job time : 20.6667 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 6, 2006, 16:13:46 ; Search time 118 seconds

(without alignments)
53.811 Million cell updates/sec

Title: US-10-791-217a-1

Perfect score: 37

Sequence: 1 VLXDDLHA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 1766

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	43.2	9	2	Q70SM2_HUMAN
2	16	43.2	9	2	O8LPT5_MAIZE
3	16	43.2	9	2	P82568_STREPY
4	15	40.5	9	2	Q9XJN0_VIVIRU
5	14	37.8	9	2	Q9FSZ2_CICAR
6	14	37.8	9	2	Q9QZAB_MOUSE
7	14	37.8	9	2	O85710_GRETR
8	14	37.8	9	2	O8UTD7_GHTVI
9	13	35.1	7	2	O99182_9SMEG
10	13	35.1	8	2	O6UTR2_CRYNV
11	13	35.1	8	2	O9HDS4_ASPL
12	13	35.1	8	2	O7M390_BALAC
13	13	35.1	8	2	O8H9K1_9CAUD
14	13	35.1	8	2	O8SBA0_BPR69
15	13	35.1	8	2	O6UC68_SOYBN
16	13	35.1	8	2	P72279_RHOGO
17	13	35.1	8	2	O51594_9Z2ZZ
18	13	35.1	9	2	O7M4R5_HUMAN
19	13	35.1	9	2	O9BQT4_HUMAN
20	13	35.1	9	2	O6UTK2_MALDO
21	13	35.1	9	2	O56SS9_SAKCA
22	13	35.1	9	2	O56ST0_9DIPS
23	13	35.1	9	2	O56ST1_9DIPS
24	13	35.1	9	2	O56ST2_9DIPS
25	13	35.1	9	2	O56ST3_VIRBP
26	13	35.1	9	2	O56ST4_9DIPS
27	13	35.1	9	2	O56ST5_9DIPS
28	13	35.1	9	2	O56ST6_9DIPS
29	13	35.1	9	2	O56ST7_VIBURNUM
30	13	35.1	9	2	O56ST8_9DIPS
31	13	35.1	9	2	O56ST9_9DIPS

32	13	35.1	9	2	O56SU1_9DIPS	O56SU1_viburnum pr
33	13	35.1	9	2	O56SU2_9DIPS	O56SU2_viburnum p1
34	13	35.1	9	2	O56SU3_9DIPS	O56SU3_viburnum od
35	13	35.1	9	2	O56SU4_9DIPS	O56SU4_viburnum nu
36	13	35.1	9	2	O56SU5_9DIPS	O56SU5_viburnum mo
37	13	35.1	9	2	O56SU6_9DIPS	O56SU6_viburnum me
38	13	35.1	9	2	O56SU7_9DIPS	O56SU7_viburnum lo
39	13	35.1	9	2	O56SU8_9DIPS	O56SU8_viburnum le
40	13	35.1	9	2	O56SU9_VIRBLN	O56SU9_viburnum la
41	13	35.1	9	2	O56SV0_VIRBLN	O56SV0_viburnum ja
42	13	35.1	9	2	O56SV1_9DIPS	O56SV1_viburnum ka
43	13	35.1	9	2	O56SV2_9DIPS	O56SV2_viburnum ju
44	13	35.1	9	2	O56SV3_9DIPS	O56SV3_viburnum ja
45	13	35.1	9	2	O56SV4_9DIPS	O56SV4_viburnum ha

ALIGNMENTS

RESULT 1					
ID	Q70SM2_HUMAN	PRELIMINARY;	PRT;	9 AA.	
AC	Q70SM2;				
DT	05-JUL-2004 (TREMBLrel. 27, Created)				
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)				
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)				
DE	Hypermethylation in cancer 1 (Fragment).				
GN	Name=HIC1;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;				
OC	Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Mammary gland;				
RA	Pinx S., Guerardel C., Deltour S., Godwin A.K., Lepince D.;				
RT	"Identification of a second G-C-rich promoter conserved in the human,				
RL	murine and rat tumor suppressor genes HIC1."				
RL	Oncogene 23:4023-4031 (2004).				
DR	EMBL; AJ550616; CAD79467.1; -; mRNA.				
FT	NON TER				
SQ	SEQUENCE 9 AA; 964 MW; 5BSR6DB1601AAA7 CRC64;				
Query Match					
Best Local Similarity 43.2%; Score 16; DB 2; Length 9;					
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;					
QY	5 DLEA 9				
DB	3 DTMEA 7				
RESULT 2					
ID	O8LPT5_MAIZE	PRELIMINARY;	PRT;	9 AA.	
AC	O8LPT5;				
DT	01-OCT-2002 (TREMBLrel. 22, Created)				
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)				
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)				
DE	Beta-expansin-like protein (Fragment).				
OS	Zea mays (Maize).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
OC	PACCB clade; Panicoideae; Andropogoneae; Zea.				
OC	NCBI_Taxid=4577;				
OC	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,				
RA	Morgante M., Rafalski J.A.;				
RL	Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AY094310; AAM21836.1; -; Genomic DNA.				
FT	NON TER				

SQ SEQUENCE 9 AA; 977 MW; 5C05B2D2CB1AAA3 CRC64;

Query Match 43.2%; Score 16; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 2.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 4 DDLLE 9
|:|:|
4 DEVUDA 9

RESULT 3

P82568_STRPY PRELIMINARY; PRT; 9 AA.

AC P82568; 01-OCT-2000 (TRENBLrel. 15, Created)

DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)

DE 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

OS Streptococcus pyogenes.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=1314;

RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.

RC STRAIN=RS4; Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,

RA Hogan D.A., Vanbogelen R.A.,

RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes

protein.";

RU Submitted (MAY-2000) to Swiss-Prot.

CC -1- MASS SPECTROMETRY: MW=22592.04; METHOD=Electrospray.

FT NON TER 1 1

FT NON TER 9 9

SQ SEQUENCE 9 AA; 1069 MW; 2A771042CB1AB2D7 CRC64;

Query Match 43.2%; Score 16; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 4 DDLLE 8
|:|:|
4 DEVIE 8

RESULT 4
O9XJNO_9VIRU PRELIMINARY; PRT; 9 AA.

AC O9XJNO; 01-NOV-1999 (TRENBLrel. 12, Created)

DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)

DE 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

OS Bacteriophage phi-10.

OC Viruses; dsRNA viruses; Cystoviridae; Cystovirus.

OX NCBI_TaxID=90889;

RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=99350412; PubMed=10419946;

RT Mindich L., Qiao X., Qiao X., Onodera S., Romanschuk M.,

RA Hoogstraaten D.;

RT "Isolation of additional bacteriophages with genomes of segmented

double-stranded RNA.";

RT J. Bacteriol. 181:4505-4508(1999).

DR EMBL; AF125675; AAD2255.1; -; Genomic_RNA.

FT NON TER 9 9

SQ SEQUENCE 9 AA; 1058 MW; 880E376A720544A CRC64;

Query Match 40.5%; Score 15; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 4 DDLLE 8

DB 2 DNILLD 6
|:|:|

RESULT 5
O9FS22_CICAR PRELIMINARY; PRT; 9 AA.

AC O9FS22; 01-MAR-2001 (TRENBLrel. 16, Created)

DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)

DE 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

OS Hypothetical protein (Fragment).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids I; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.

OX NCBI_TaxID=3827;

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Etliolated epicotyls;

RA Dopico B., Jimenez T., Labrador B.;

RU Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL; AJ299069; CAC10216.1; -; mRNA.

FT NON TER 1 1

SQ SEQUENCE 9 AA; 990 MW; 9441BDDA7272B8E CRC64;

Query Match 37.8%; Score 14; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 LLEA 9
|:|:|
4 LLDA 7

RESULT 6
O9QZAB_MOUSE PRELIMINARY; PRT; 9 AA.

AC O9QZAB; 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DE 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

OS C-type lectin DCL1 (Fragment).

GN Name=Clec21; Synonyms=Dcl1;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RP NUCLEOTIDE SEQUENCE.

RA Goretzki K., Huang X., Tseng S.-Y., Rattis F., Pardoll D., Tsuchiya H.;

RU Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF192526; AAF04843.1; -; Genomic_DNA.

DR MGI; MGI:2136650; Dcl1.

DR GO; GO:000897; C:external side of plasma membrane; IDA.

DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0046703; F:natural killer cell lectin-like receptor bi. . .; IDA.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); TAS.

KW lectin.

FT NON TER 9 9

SQ SEQUENCE 9 AA; 994 MW; 342161AB172EBAB7 CRC64;

Query Match 37.8%; Score 14; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 DLLE 8
|:|:|
3 DLLE 6

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RESULT 7
ID 085710_9RETR PRELIMINARY; PRT; 9 AA.
AC 085710;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Pol protein (Fragment).
OS Rous sarcoma virus.
OC Viruses; Retroviral viruses; Retroviridae; Alpharetrovirus.
NCBI_TaxID=11886;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=84115080; PubMed=6319754;
RA Lemner T.L., Hanafusa H.,
RT "DNA sequence of the Bryan high-titer strain of Rous sarcoma virus:
RT extent of env deletion and possible genealogical relationship with
RT other viral strains.";
RL J. Virol. 49:549-556(1984).
DR EMBL; K03365; AAA42557.1; -; Genomic_RNA.
FT NON TER
SQ SEQUENCE 9 AA; 949 MW; 94AA144DDDD731AA CRC64;

Query Match
Best Local Similarity 37.8%; Score 14; DB 2; Length 9;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 DDLRA 9
Db 1 EDTLAA 6

RESULT 8
ID 08UTD7_9HIV1 PRELIMINARY; PRT; 9 AA.
AC 08UTD7;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Vpu protein.
GN Name=vpu;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus;
OC Primate lentivirus group.
NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=21988475; PubMed=11991972;
RX DOI=10.1128/JVI.76.11.5435-5451.2002;
RA Novitsky V., Smith U.R., Gilbert P., McLane M.F., Chigwedere P.,
RA Williamson C., Nhung U.T., Klein I., Chang S.-Y., Peter T., Thior I.,
RA Foley B.T., Gaoletke S., Rybak N., Gassetts S., Vamberg F.,
RA Marlink R., Lee T.-H., Essex M.;
RT "Human immunodeficiency virus type 1 subtype C molecular phylogeny:
RT consensus sequence for an AIDS vaccine design?";
RL J. Virol. 76:5435-5451(2002).
RN NUCLEOTIDE SEQUENCE.
RP Novitsky V.A., McLane M.F., Chigwedere P., Nhung U.T., Klein I.,
RA Chang S.-Y., Peter T., Thior I., Rybak N., Gassetts S., Vamberg F.,
RA Marlink R., Lee T.-H., Essex M.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF443091; AAL34712.1; -; Genomic DNA.
SQ SEQUENCE 9 AA; 1102 MW; 188BD40B17272440 CRC64;

Query Match
Best Local Similarity 37.8%; Score 14; DB 2; Length 9;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DDLR 8
Db 1 EDTLAA 6

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Db 3 NMLE 6

RESULT 9
ID 099182_9SMEG PRELIMINARY; PRT; 7 AA.
AC 099182;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cytochrome oxidase I (Fragment).
GN Name=COI;
OS Gnatholebias zonatus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percormorpha; Atherinomorphi;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Gnatholebias.
NCBI_TaxID=135316;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=20072828; PubMed=10603257; DOI=10.1006/mpev.1999.0656;
RA Murphy W.D., Thomson J.E., Collier G.E.;
RT "Phylogeny of the Neotropical killifish family Rivulidae
RT (Cyprinodontiformes, Aplocheilidae) inferred from mitochondrial DNA
RT sequences.";
RL Mol. Phylogenet. Evol. 13:289-301(1999).
DR EMBL; AF002591; AAD01074.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 7 AA; 899 MW; 672721F6CB572030 CRC64;

Query Match
Best Local Similarity 35.1%; Score 13; DB 2; Length 7;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VLXDDL 7
Db 1 ILYQHL 7

RESULT 10
ID 06UTR2_CRYNV PRELIMINARY; PRT; 8 AA.
AC 06UTR2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Squalene monooxygenase (EC 1.14.99.7) (Fragment).
GN Name=ERGL1;
OS Cyrtococcus neofornans var. grubii H99.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
NCBI_TaxID=235443;
RN NUCLEOTIDE SEQUENCE.
RP Stuart L.T., Allen A., Dietrich F.S.;
RC STRAIN=H99;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY376718; AA088127.1; -; mRNA.
DR GO; GO:0004506; F:squalene monooxygenase activity; IEA.
KW Monooxygenase; Oxidoreductase.
FT NON TER
SQ SEQUENCE 8 AA; 811 MW; 046776AAB1DD727 CRC64;

Query Match
Best Local Similarity 35.1%; Score 13; DB 2; Length 8;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDD 5
Db 1 ILAED 5

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RESULT 11
Q9HDS4 ASPFL PRELIMINARY; PRT; 8 AA.
AC Q9HDS4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE TIPC polypeptide (Fragment).
GN Name=trpC;
OS Aspergillus flavus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocommataceae; mitosporic Trichocommataceae; Aspergillus.
OK NCBI_TaxId=5059;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A55;
RX MEDLINE=2117363; PubMed=11273679; DOI=10.1006/fgbi.2000.1215;
RA Gelsner D.M., Dörner J.W., Horn B.W., Taylor J.W.,
RT "The phylogenetics of mycotoxin and sclerotium production in
RT Aspergillus flavus and Aspergillus oryzae."
RL Fungal Genet. Biol. 31:169-179(2000).
DR EMBL; AF261861; AAG16135.1; -; Genomic_DNA.
KW Polypeptide.
FT NON_TER
SQ SEQUENCE 8 AA; 807 MW; F3B2C72AB5B87DD6 CRC64;

Query Match 35.1%; Score 13; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 DLXD 8
DB 5 ILTD 8

RESULT 12
Q7M390 BALAC PRELIMINARY; PRT; 8 AA.
AC Q7M390;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE Trypsin (EC 3.4.21.4) precursor (Fragment).
OS Balaenoptera acutorostrata (Mink whale) (Lesser rorqual).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Mysticeti; Balaenopteridae; Balaenoptera.
OK NCBI_TaxId=9767;
RN [1]
RP PROTEIN SEQUENCE.
RA Briceux-Gregoire S., Schyns R., Florkin M., Emmens M., Welling G.W.,
RA Beintema J.J.;
RT "N-terminal amino acid sequence of trypsinogen from the lesser
RT rorqual, Balaenoptera acutorostrata (Cetacea). Simultaneous isolation
RT of trypsinogen, chymotrypsinogen and ribonuclease from pancreas."
RL Biochim. Biophys. Acta 386:244-255(1975).
RN [2]
RP PROTEIN SEQUENCE.
RX PubMed=1125273;
RA Briceux-Gregoire S., Schyns R., Florkin M., Emmens M., Welling G.W.,
RA Beintema J.J.;
RT "N-terminal amino acid sequence of trypsinogen from the lesser
RT rorqual, Balaenoptera acutorostrata (Cetacea). Simultaneous isolation
RT of trypsinogen, chymotrypsinogen and ribonuclease from pancreas."
RL Biochim. Biophys. Acta 386:244-255(1975).
DR PIR; A61328; A61328.
DR GO; GO:0004295; F:trypsin activity; IEA.
FT NON_TER
SQ SEQUENCE 8 AA; 964 MW; 8D3AAAAAAA04769 CRC64;

Query Match 35.1%; Score 13; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXDD 5
DB 3 IDDD 6

RESULT 13
Q8H9K1_GCAUD PRELIMINARY; PRT; 8 AA.
AC Q8H9K1;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE Gp30.2 protein (Fragment).
GN Name=30.2;
OS Bacteriophage I210.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OK NCBI_TaxId=192973;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kolesinskiene G., Nivinskas R.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ458400; CAD30256.1; -; Genomic_DNA.
FT NON_TER
SQ SEQUENCE 8 AA; 918 MW; F3B1A72041B76336 CRC64;

Query Match 35.1%; Score 13; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXD 4
DB 5 ILTD 8

RESULT 14
Q8SBJ0_BPR69 PRELIMINARY; PRT; 8 AA.
AC Q8SBJ0;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE Gp30.2 (Fragment).
GN Name=30.2;
OS Bacteriophage RB69.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OK NCBI_TaxId=12353;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Plesinsiene L., Kolesinskiene G., Truncate L., Zajackauskaite A.,
RA Nivinskas R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ439452; CAD28423.1; -; Genomic_DNA.
FT NON_TER
SQ SEQUENCE 8 AA; 918 MW; F3B1A72041B76336 CRC64;

Query Match 35.1%; Score 13; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXD 4
DB 5 ILTD 8

RESULT 15
Q6JC68_SOYBN PRELIMINARY; PRT; 8 AA.
ID Q6JC68_SOYBN

AC Q6JC68;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Isoflavone synthase 1 (Fragment).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OC NCBI_TaxID=3847;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15356384; DOI=10.1023/B:PLAN.0000040814.28507.35;
 RA Subramanian S., Hu X., Lu G., Odell J.T., Yu O.;
 RT "The promoters of two isoflavone synthase genes respond differentially
 RL to nodulation and defense signals in transgenic soybean roots.";
 RL Plant Mol. Biol. 54:623-639(2004).
 DR EMBL; AY530096; MAF01227.1; -; Genomic_DNA.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 859 MW; F1772DD72B172726 CRC64;

Query Match 35.1%; Score 13; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 LLE 8
 |||
 Db 2 LLE 4

Search completed: April 6, 2006, 16:25:08
 Job time : 120 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 6, 2006, 16:25:31 ; Search time 27.333 Seconds
(without alignments)
27.222 Million cell updates/sec

Title: US-10-791-217a-1

Perfect score: 37

Sequence: 1 VLXDDLEA 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 111694

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5 COMB.pep.*
- 2: /cgn2_6/prodata/1/1aa/6 COMB.pep.*
- 3: /cgn2_6/prodata/1/1aa/7 COMB.pep.*
- 4: /cgn2_6/prodata/1/1aa/8 COMB.pep.*
- 5: /cgn2_6/prodata/1/1aa/9 COMB.pep.*
- 6: /cgn2_6/prodata/1/1aa/10 COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	97.3	9	US-09-269-250E-18	Sequence 18, Appl
2	36	97.3	9	US-09-269-250E-20	Sequence 20, Appl
3	36	97.3	9	US-09-269-250E-29	Sequence 29, Appl
4	36	97.3	9	US-09-489-760-1	Sequence 1, Appl
5	36	97.3	9	US-09-489-760-2	Sequence 2, Appl
6	36	97.3	9	US-09-489-760-5	Sequence 5, Appl
7	36	97.3	9	US-09-269-250E-38	Sequence 38, Appl
8	36	97.3	9	US-09-556-419-14	Sequence 14, Appl
9	36	97.3	9	US-09-744-549-15	Sequence 15, Appl
10	36	97.3	9	US-10-394-980-421	Sequence 421, Appl
11	36	97.3	9	US-10-394-980-464	Sequence 464, Appl
12	36	97.3	9	US-08-459-568-20	Sequence 20, Appl
13	36	97.3	9	US-08-399-411-20	Sequence 20, Appl
14	36	97.3	9	US-08-516-859A-20	Sequence 20, Appl
15	36	97.3	9	US-09-586-472-20	Sequence 20, Appl
16	36	97.3	9	US-09-528-706-20	Sequence 20, Appl
17	36	97.3	9	US-08-459-568-75	Sequence 75, Appl
18	36	97.3	9	US-08-399-411-75	Sequence 75, Appl
19	36	97.3	9	US-08-516-859A-75	Sequence 75, Appl
20	36	97.3	9	US-09-586-472-75	Sequence 75, Appl
21	36	97.3	9	US-09-528-706-75	Sequence 75, Appl
22	36	97.3	9	US-08-459-568-78	Sequence 78, Appl
23	36	97.3	9	US-08-399-411-78	Sequence 78, Appl
24	36	97.3	9	US-08-516-859A-78	Sequence 78, Appl
25	36	97.3	9	US-09-586-472-78	Sequence 78, Appl
26	36	97.3	9	US-09-528-706-78	Sequence 78, Appl
27	36	97.3	9	US-08-459-568-78	Sequence 78, Appl

28	21	56.8	9	US-09-217-609A-11	Sequence 11, Appl
29	21	56.8	9	US-08-873-235B-11	Sequence 11, Appl
30	21	56.8	9	US-09-586-472-72	Sequence 72, Appl
31	21	56.8	9	US-09-586-472-78	Sequence 78, Appl
32	21	56.8	9	US-09-528-706-72	Sequence 72, Appl
33	21	56.8	9	US-09-528-706-78	Sequence 78, Appl
34	21	56.8	9	US-09-489-760-4	Sequence 4, Appl
35	21	56.8	9	US-09-025-819-11	Sequence 11, Appl
36	21	56.8	9	US-09-808-126-11	Sequence 11, Appl
37	21	56.8	9	US-09-803-951-11	Sequence 11, Appl
38	21	56.8	9	US-08-747-599A-47	Sequence 47, Appl
39	21	56.8	9	US-08-747-599A-50	Sequence 50, Appl
40	21	56.8	9	US-08-747-599A-51	Sequence 51, Appl
41	21	56.8	9	US-08-974-549A-373	Sequence 373, Appl
42	21	56.8	9	US-08-912-951-140	Sequence 140, Appl
43	21	56.8	9	US-09-402-181B-373	Sequence 373, Appl
44	21	56.8	9	US-09-721-456-373	Sequence 373, Appl
45	21	56.8	9	US-09-187-859-1186	Sequence 1186, Appl

ALIGNMENTS

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RESULT 1
US-09-269-250E-18
; Sequence 18, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elia
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-18

Query Match
Best Local Similarity 97.3%; Score 36; DB 2; Length 9;
Matches 8; Conservative 0; Mismatches 1; Indels 0;

QY 1 VLXDDLEA 9
DB 1 VLXDDLEA 9

RESULT 2
US-09-269-250E-20
; Sequence 20, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elia
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-20

Query Match
Best Local Similarity 97.3%; Score 36; DB 2; Length 9;
Matches 8; Conservative 0; Mismatches 1; Indels 0;

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Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
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Db 1 VLHDDLLEA 9

RESULT 3

US-09-269-250E-29
; Sequence 29, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
US-09-269-250E-29

Query Match 97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
|||
Db 1 VLXDDLLEA 9

RESULT 4

US-09-489-760-1
; Sequence 1, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leiden
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Histocompatibility antigen
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (3)
; OTHER INFORMATION: AMINO ACID X REPRESENTS A HISTIDINE OR AN ARGININE
; OTHER INFORMATION: RESIDUE
US-09-489-760-1

Query Match 97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
|||
Db 1 VLXDDLLEA 9

Db 1 VLXDDLLEA 9

RESULT 5

US-09-489-760-2
; Sequence 2, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leiden
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Victor H
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Histocompatibility antigen
US-09-489-760-2

Query Match 97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
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Db 1 VLHDDLLEA 9

RESULT 6

US-09-489-760-5
; Sequence 5, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leiden
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Victor H
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: KIAA0223 partial complementary DNA
US-09-489-760-5

Query Match 97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
|||
Db 1 VLHDDLLEA 9

RESULT 7

US-09-269-250E-38
; Sequence 38, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa

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; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN
US-09-269-250E-38
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Query Match          62.2%; Score 23; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      5 DDLLE 9
      |||||
Db      4 DDLLE 8
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RESULT 8
US-08-556-419-14
; Sequence 14, Application US/08556419C
; Patent No. 6093549
; GENERAL INFORMATION:
; APPLICANT: Ross, Christopher
; APPLICANT: Li, Xiao-Jiang
; APPLICANT: Li, Shi-Hua
; APPLICANT: Sharp, Alan
; APPLICANT: Lanahan, Anthony
; APPLICANT: Worley, Paul
; APPLICANT: Snyder, Solomon
; TITLE OF INVENTION: Huntingtin-associated protein
; FILE REFERENCE: 01107.52271
; CURRENT APPLICATION NUMBER: US/08/556,419C
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-08-556-419-14
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Query Match          59.5%; Score 22; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      4 DDLLE 8
      |||||
Db      1 DDLLE 5
```

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RESULT 9
US-09-744-549-15
; Sequence 15, Application US/09744549
; Patent No. 6664232
; GENERAL INFORMATION:
; APPLICANT: Itoh, Kyogo et al.
; TITLE OF INVENTION: HLA-A2-restricted Tumor Antigen Peptides Derived From SART-1
; FILE REFERENCE: 0020-4808P
; CURRENT APPLICATION NUMBER: US/09/744,549
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: JP H10-212940
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-744-549-15
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Query Match          59.5%; Score 22; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY      1 VLXDDL 7
      |||||
Db      3 VRADLLE 9
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RESULT 10
US-10-394-980-421
; Sequence 421, Application US/10394980
; Patent No. 6908740
; GENERAL INFORMATION:
; APPLICANT: Vandekerckhove, Joel
; APPLICANT: Gevaert, Kris
; TITLE OF INVENTION: METHODS AND APPARATUS FOR GEL-FREE QUALITATIVE AND
; TITLE OF INVENTION: QUANTITATIVE PROTEOME ANALYSIS, AND USES THEREFOR
; FILE REFERENCE: VBV-001
; CURRENT APPLICATION NUMBER: US/10/394,980
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: PCT/EP02/03368
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US60/278,171
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US60/318,749
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/323,999
; PRIOR FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 421
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: FR10 - 1624,68
US-10-394-980-421
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Query Match          59.5%; Score 22; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 LXXDDL 8
      |||||
Db      3 LXXDDL 9
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```
RESULT 11
US-10-394-980-464
; Sequence 464, Application US/10394980
; Patent No. 6908740
; GENERAL INFORMATION:
; APPLICANT: Vandekerckhove, Joel
; APPLICANT: Gevaert, Kris
; TITLE OF INVENTION: METHODS AND APPARATUS FOR GEL-FREE QUALITATIVE AND
; TITLE OF INVENTION: QUANTITATIVE PROTEOME ANALYSIS, AND USES THEREFOR
; FILE REFERENCE: VBV-001
; CURRENT APPLICATION NUMBER: US/10/394,980
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: PCT/EP02/03368
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US60/278,171
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US60/318,749
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/323,999
; PRIOR FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 464
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LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: Table XIX - 1624.68
US-10-394-980-464

Query Match 59.5%; Score 22; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LDDLE 8
Db 3 LDDLE 9

RESULT 12
US-08-459-568-20

Sequence 20, Application US/08459568
Patent No. 5811304

GENERAL INFORMATION:

APPLICANT: Huang, Shi

TITLE OF INVENTION: Retinoblastoma Protein - Interacting

TITLE OF INVENTION: Zinc Finger Proteins

NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,568

FILING DATE: 02-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/399,411

FILING DATE: 06-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LJ 1264

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-459-568-20

Query Match 56.8%; Score 21; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDLLE 8
Db 1 EDLLE 5

RESULT 13
US-08-399-411-20

Sequence 20, Application US/08399411

Patent No. 5831008

GENERAL INFORMATION:

APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA

Query Match 59.5%; Score 22; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LDDLE 8
Db 3 LDDLE 9

RESULT 12
US-08-459-568-20

Sequence 20, Application US/08459568
Patent No. 5811304

GENERAL INFORMATION:

APPLICANT: Huang, Shi

TITLE OF INVENTION: Retinoblastoma Protein - Interacting

TITLE OF INVENTION: Zinc Finger Proteins

NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/399,411

FILING DATE: 06-MAR-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/399,411

FILING DATE: 06-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LJ 1264

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-399-411-20

Query Match 56.8%; Score 21; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDLLE 8
Db 1 EDLLE 5

RESULT 14
US-08-516-859A-20

Sequence 20, Application US/08516859A

Patent No. 6069231

GENERAL INFORMATION:

APPLICANT: Huang, Shi

TITLE OF INVENTION: Retinoblastoma Protein - Interacting

TITLE OF INVENTION: Zinc Finger Proteins

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/516,859A

FILING DATE: 18-AUG-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/399,411

FILING DATE: 06-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/292,683

FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1776
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-516-859A-20

Query Match 56.8%; Score 21; DB 2; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8
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Db 1 EDLLE 5

RESULT 15

US-09-586-472-20
Sequence 20, Application US/09586472
Patent No. 632335
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/586,472
FILING DATE: 01-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/528,706
FILING DATE: 17-MAR-2000
APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 4130
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-586-472-20

Query Match 56.8%; Score 21; DB 2; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8
: |||
Db 1 EDLLE 5

Search completed: April 6, 2006, 16:27:37
Job time : 27.6667 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:44:31 ; Search time 90.3333 Seconds
(without alignments)
41.629 Million cell updates/sec

Title: US-10-791-217A-1

Perfect score: 37

Sequence: 1 VLXDDLRA 9

Scoring table: BLOSUM62

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 180914

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	97.3	9	4 US-10-623-176-1	Sequence 1, Appl
2	36	97.3	9	4 US-10-623-176-2	Sequence 2, Appl
3	36	97.3	9	4 US-10-623-176-10	Sequence 10, Appl
4	36	97.3	9	4 US-10-791-217-1	Sequence 1, Appl
5	36	97.3	9	4 US-10-791-217-2	Sequence 2, Appl
6	36	97.3	9	4 US-10-791-217-5	Sequence 5, Appl
7	36	97.3	9	5 US-10-861-335-1	Sequence 1, Appl
8	36	97.3	9	6 US-11-007-740-18	Sequence 18, Appl
9	36	97.3	9	6 US-11-007-740-29	Sequence 29, Appl
10	36	97.3	9	4 US-11-007-740-42	Sequence 42, Appl
11	32	86.5	9	4 US-10-623-176-41	Sequence 41, Appl
12	32	86.5	9	4 US-10-623-176-42	Sequence 42, Appl
13	32	86.5	9	4 US-10-623-176-45	Sequence 45, Appl
14	32	86.5	9	4 US-10-623-176-46	Sequence 46, Appl
15	29	78.4	9	4 US-10-623-176-47	Sequence 47, Appl
16	29	78.4	9	4 US-10-623-176-48	Sequence 48, Appl
17	27	73.0	9	4 US-10-623-176-23	Sequence 23, Appl
18	27	73.0	9	4 US-10-623-176-40	Sequence 40, Appl
19	23	62.2	8	6 US-10-623-176-15	Sequence 15, Appl
20	23	62.2	8	6 US-11-007-740-38	Sequence 38, Appl
21	23	62.2	9	3 US-09-834-765-132	Sequence 132, App
22	23	62.2	9	4 US-09-834-765-349	Sequence 349, App
23	23	62.2	9	4 US-10-623-176-3	Sequence 3, Appl
24	23	62.2	9	4 US-10-623-176-4	Sequence 4, Appl
25	23	62.2	9	4 US-10-623-176-5	Sequence 5, Appl
26	22	59.5	9	4 US-10-119-536A-109	Sequence 109, App
27	22	59.5	9	4 US-10-394-980-421	Sequence 421, App

28	22	59.5	9	4 US-10-394-980-464	Sequence 464, App
29	22	59.5	9	5 US-10-275-652-50	Sequence 50, Appl
30	22	59.5	9	5 US-10-952-557-421	Sequence 421, Appl
31	22	59.5	9	5 US-10-952-557-464	Sequence 464, App
32	22	59.5	9	5 US-10-996-306-109	Sequence 109, App
33	21	56.8	9	3 US-09-833-203-54	Sequence 54, Appl
34	21	56.8	9	4 US-10-057-475B-10608	Sequence 10608, A
35	21	56.8	9	4 US-10-057-475B-10813	Sequence 10813, A
36	21	56.8	9	4 US-10-154-884B-10608	Sequence 10608, A
37	21	56.8	9	4 US-10-154-884B-10813	Sequence 10813, A
38	21	56.8	9	4 US-10-623-176-14	Sequence 14, Appl
39	21	56.8	9	4 US-10-791-217-4	Sequence 4, Appl
40	21	56.8	9	4 US-10-809-790-23	Sequence 23, Appl
41	21	56.8	9	5 US-10-999-364-73	Sequence 73, Appl
42	21	56.8	9	6 US-11-007-740-40	Sequence 40, Appl
43	20	54.1	5	4 US-10-166-225A-168	Sequence 168, App
44	20	54.1	5	4 US-10-166-225A-169	Sequence 169, App
45	20	54.1	5	4 US-10-166-225A-170	Sequence 170, App

ALIGNMENTS

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RESULT 1
US-10-623-176-1
; Sequence 1, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhardt, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-604705
; CURRENT APPLICATION NUMBER: US/10/623,176
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; OTHER INFORMATION: wherein X can be R or H
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(9)
; US-10-623-176-1

Query Match          97.3%; Score 36; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 VLXDDLRA 9
Db      1 VLXDDLRA 9

RESULT 2
US-10-623-176-2
; Sequence 2, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Els A.J.M.
; APPLICANT: Hunt, Donald F.

```

```

; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-2

Query Match      97.3%; Score 36; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      1 VLXDDLLEA 9
Db      1 VLXDDLLEA 9

RESULT 3
US-10-623-176-10
; Sequence 10, Application US/10623176
; Publication No. US2004009246A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-10

Query Match      97.3%; Score 36; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      1 VLXDDLLEA 9
Db      1 VLXDDLLEA 9
```

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Db      1 VLXDDLLEA 9

RESULT 4
US-10-791-217-1
; Sequence 1, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/10/791,217
; PRIOR FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: obtained from histocompatibility antigen
; NAME/KEY: MISC FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa is HISTIDINE OR ARGININE RESIDUE
US-10-791-217-1

Query Match      97.3%; Score 36; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 VLXDDLLEA 9
Db      1 VLXDDLLEA 9

RESULT 5
US-10-791-217-2
; Sequence 2, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/10/791,217
; PRIOR FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: obtained from histocompatibility antigen
US-10-791-217-2

Query Match      97.3%; Score 36; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
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OY 1 VLXDDLLEA 9
|||
Db 1 VLHDDLLEA 9

RESULT 6
US-10-791-217-5
; Sequence 5, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elia A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/10/791,217
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: obtained from KIA0223 partial complementary DNA
US-10-791-217-5

Query Match 97.3%; Score 36; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLXDDLLEA 9
|||
Db 1 VLHDDLLEA 9

RESULT 7
US-10-861-335-1
; Sequence 1, Application US/10861335
; Publication No. US20050031612A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elia A.J.M.
; TITLE OF INVENTION: Minor histocompatibility antigen HA-1: target antigen for immunot
; FILE REFERENCE: 2183-6479US
; CURRENT APPLICATION NUMBER: US/10/861,335
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: PCT/NL02/00791
; PRIOR FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: EP 01204704.9
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HA-1 peptide
US-10-861-335-1

Query Match 97.3%; Score 36; DB 5; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLXDDLLEA 9
|||
Db 1 VLHDDLLEA 9

RESULT 8
US-11-007-740-18
; Sequence 18, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elia
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 2799/58994-A
; CURRENT APPLICATION NUMBER: US/11/007,740
; CURRENT FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: 09/269,250
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-18

Query Match 97.3%; Score 36; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLXDDLLEA 9
|||
Db 1 VLHDDLLEA 9

RESULT 9
US-11-007-740-20
; Sequence 20, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elia
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 2799/58994-A
; CURRENT APPLICATION NUMBER: US/11/007,740
; CURRENT FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: 09/269,250
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-20

Query Match 97.3%; Score 36; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLXDDLLEA 9
|||
Db 1 VLHDDLLEA 9

RESULT 10
US-11-007-740-29
; Sequence 29, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elia
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 2799/58994-A
; CURRENT APPLICATION NUMBER: US/11/007,740
; CURRENT FILING DATE: 2004-12-08

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;; PRIOR APPLICATION NUMBER: 09/269,250
;; PRIOR FILING DATE: 1999-05-21
;; NUMBER OF SEQ ID NOS: 40
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 29
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (3)..(3)
;; OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
US-11-007-740-29
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Query Match          97.3%; Score 36; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 VLXDDLEA 9
Db      1 VLXDDLEA 9
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RESULT 11

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US-10-623-176-41
; Sequence 41, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT FILING DATE: 2003-07-18
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-41
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Query Match          86.5%; Score 32; DB 4; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 VLXDDLE 8
Db      2 VLHDDLE 9
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RESULT 12

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US-10-623-176-42
; Sequence 42, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
```

```
;; TITLE OF INVENTION: HA-1 epitopes and uses thereof
;; FILE REFERENCE: 2183-6047US
;; CURRENT APPLICATION NUMBER: US/10/623,176
;; CURRENT FILING DATE: 2003-07-18
;; PRIOR APPLICATION NUMBER: 09/489,760
;; PRIOR FILING DATE: 2000-01-21
;; PRIOR APPLICATION NUMBER: EP 97202303.0
;; PRIOR FILING DATE: 1997-07-23
;; PRIOR APPLICATION NUMBER: PCT/NL98/00424
;; PRIOR FILING DATE: 1998-07-23
;; PRIOR APPLICATION NUMBER: JP 2000-504165
;; PRIOR FILING DATE: 2000-01-24
;; NUMBER OF SEQ ID NOS: 77
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 42
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (1)..(9)
US-10-623-176-42
```

```
Query Match          86.5%; Score 32; DB 4; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
Qy      1 VLXDDLE 8
Db      2 VLHDDLE 9
```

RESULT 13

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US-10-623-176-45
; Sequence 45, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-45
```

```
Query Match          86.5%; Score 32; DB 4; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      2 LXDLDLEA 9
```

Db 1 LHDDLLEA 8

RESULT 14

US-10-623-176-46
 ; Sequence 46, Application US/10623176
 ; Publication No. US20040092446A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goulmy, Els A.J.M.
 ; APPLICANT: Hunt, Donald F.
 ; APPLICANT: Engelhard, Victor H.
 ; TITLE OF INVENTION: HA-1 epitopes and uses thereof
 ; FILE REFERENCE: 2183-6047US
 ; CURRENT APPLICATION NUMBER: US/10/623,176
 ; PRIOR FILING DATE: 2003-07-18
 ; PRIOR APPLICATION NUMBER: 09/489,760
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: EP 97202303.0
 ; PRIOR FILING DATE: 1997-07-23
 ; PRIOR APPLICATION NUMBER: PCT/NL98/00424
 ; PRIOR FILING DATE: 1998-07-23
 ; PRIOR APPLICATION NUMBER: JP 2000-504165
 ; PRIOR FILING DATE: 2000-01-24
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 46
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
 ; NAME/KEY: SITE
 ; LOCATION: (1)..(9)
 US-10-623-176-46

Query Match 86.5%; Score 32; DB 4; Length 9;
 Best Local Similarity 87.5%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKDDLLEA 9
 Db 1 LHDDLLEA 8

RESULT 15

US-10-623-176-47
 ; Sequence 47, Application US/10623176
 ; Publication No. US20040092446A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goulmy, Els A.J.M.
 ; APPLICANT: Hunt, Donald F.
 ; APPLICANT: Engelhard, Victor H.
 ; TITLE OF INVENTION: HA-1 epitopes and uses thereof
 ; FILE REFERENCE: 2183-6047US
 ; CURRENT APPLICATION NUMBER: US/10/623,176
 ; PRIOR FILING DATE: 2003-07-18
 ; PRIOR APPLICATION NUMBER: 09/489,760
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: EP 97202303.0
 ; PRIOR FILING DATE: 1997-07-23
 ; PRIOR APPLICATION NUMBER: PCT/NL98/00424
 ; PRIOR FILING DATE: 1998-07-23
 ; PRIOR APPLICATION NUMBER: JP 2000-504165
 ; PRIOR FILING DATE: 2000-01-24
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 47
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide

FEATURE:
 NAME/KEY: SITE
 LOCATION: (1)..(9)
 US-10-623-176-47

Query Match 78.4%; Score 29; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDILLEA 9
 Db 2 DDILLEA 7

Search completed: April 6, 2006, 16:50:29
 Job time : 91.3333 secs

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OM protein - protein search, using sw model

Run on: April 6, 2006, 16:46:11 / Search time 12.3333 Seconds
(without alignments)
22.762 Million cell updates/sec

Title: US-10-791-217A-1

Perfect score: 37
Sequence: 1 VLXDDLRA 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 38721

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New:*
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3: /SIDS5/prodata/2/pubppa/US07_NEW_PUB.pep:*
4: /SIDS5/prodata/2/pubppa/PCT_NEW_PUB.pep:*
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6: /SIDS5/prodata/2/pubppa/US10_NEW_PUB.pep:*
7: /SIDS5/prodata/2/pubppa/US11_NEW_PUB.pep:*
8: /SIDS5/prodata/2/pubppa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	97.3	9	US-11-010-748A-11	Sequence 11, Appl
2	36	97.3	9	US-11-010-748A-12	Sequence 12, Appl
3	21	56.8	9	US-10-927-435-63	Sequence 63, Appl
4	21	56.8	9	US-10-927-634-63	Sequence 63, Appl
5	20	54.1	5	US-11-129-143-168	Sequence 168, App
6	20	54.1	5	US-11-129-143-169	Sequence 169, App
7	20	54.1	5	US-11-129-143-170	Sequence 170, App
8	20	54.1	5	US-11-129-143-171	Sequence 171, App
9	20	54.1	5	US-11-129-143-172	Sequence 172, App
10	20	54.1	5	US-11-129-143-173	Sequence 173, App
11	20	54.1	7	US-10-982-440-126	Sequence 126, App
12	20	54.1	8	US-11-021-305-62	Sequence 62, Appl
13	20	54.1	8	US-11-021-305-65	Sequence 65, Appl
14	20	54.1	8	US-11-021-305-66	Sequence 66, Appl
15	19	51.4	6	US-11-207-078-373	Sequence 373, App
16	19	51.4	7	US-11-225-686-2954	Sequence 2954, App
17	19	51.4	7	US-11-225-686-3877	Sequence 3877, App
18	19	51.4	7	US-11-225-686-3914	Sequence 3914, App
19	19	51.4	7	US-11-225-686-3915	Sequence 3915, App
20	19	51.4	7	US-11-225-686-3916	Sequence 3916, App
21	19	51.4	7	US-11-225-686-3932	Sequence 3932, App
22	19	51.4	7	US-11-225-686-3941	Sequence 3941, App
23	19	51.4	7	US-11-202-009-2954	Sequence 2954, App
24	19	51.4	7	US-11-202-009-3877	Sequence 3877, App
25	19	51.4	7	US-11-202-009-3914	Sequence 3914, App

26	19	51.4	7	US-11-202-009-3915	Sequence 3915, App
27	19	51.4	7	US-11-202-009-3916	Sequence 3916, App
28	19	51.4	7	US-11-202-009-3932	Sequence 3932, App
29	19	51.4	7	US-11-202-009-3941	Sequence 3941, App
30	19	51.4	7	US-10-073-301A-7	Sequence 7, Appl1
31	19	51.4	9	US-10-989-767A-39	Sequence 39, Appl1
32	19	51.4	9	US-10-927-435-62	Sequence 62, Appl1
33	19	51.4	9	US-10-927-435-62	Sequence 62, Appl1
34	19	51.4	9	US-11-203-137-7	Sequence 7, Appl1
35	18	48.6	7	US-11-096-706-88	Sequence 88, Appl1
36	18	48.6	8	US-11-267-631-42	Sequence 42, Appl1
37	18	48.6	9	US-10-981-873-24	Sequence 24, Appl1
38	18	48.6	9	US-10-997-759-29	Sequence 29, Appl1
39	18	48.6	9	US-10-895-064-1363	Sequence 1363, App
40	18	48.6	9	US-10-989-767A-219	Sequence 219, App
41	18	48.6	9	US-10-989-767A-565	Sequence 565, App
42	18	48.6	9	US-11-234-786-338	Sequence 338, App
43	18	48.6	9	US-11-129-741-1363	Sequence 1363, App
44	17	45.9	6	US-11-129-143-163	Sequence 163, App
45	17	45.9	7	US-11-129-143-164	Sequence 164, App

ALIGNMENTS

RESULT 1
US-11-010-748A-11
Sequence 11, Application US/11010748A
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMATTER, Wolfgang
APPLICANT: MOLL, Heidrun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
FILE REFERENCE: MER-136
CURRENT APPLICATION NUMBER: US/11/010,748A
PRIOR FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/EP03/06251
PRIOR FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: EP02013423.5
PRIOR FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 926
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(9)
OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
US-11-010-748A-11

Query Match 97.3%; Score 36; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLRA 9
DB 1 VLXDDLRA 9

RESULT 2
US-11-010-748A-12
Sequence 12, Application US/11010748A
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMATTER, Wolfgang
APPLICANT: MOLL, Heidrun
APPLICANT: SCHARM, Burkhard

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(9)
; OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T
; OTHER INFORMATION: ell epitopes
US-11-010-748A-12

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Query Match          97.3%; Score 36; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 VLXDDLEA 9
       |||||
Db      1 VLRDDLEA 9

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RESULT 3
US-10-927-435-63
; Sequence 63, Application US/10927435
; Publication No. US20060045884A1
; GENERAL INFORMATION:
; APPLICANT: MOLLEREM, JEFFREY
; TITLE OF INVENTION: VACCINES FOR AUTOIMMUNE AND INFECTIOUS DISEASE
; FILE REFERENCE: UTSC:788USC2
; CURRENT APPLICATION NUMBER: US/10/927,435
; CURRENT FILING DATE: 2004-08-26
; PRIOR APPLICATION NUMBER: 60/489,238
; PRIOR FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-927-435-63

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Query Match          56.8%; Score 21; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 VLXDDLE 8
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Db      1 ILDDWLE 8

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RESULT 4
US-10-927-634-63
; Sequence 63, Application US/10927634
; Publication No. US20060045884A1
; GENERAL INFORMATION:
; APPLICANT: MOLLEREM, JEFFREY
; TITLE OF INVENTION: ANTI-CANCER VACCINES
; FILE REFERENCE: UTSC:788USC1
; CURRENT APPLICATION NUMBER: US/10/927,634
; CURRENT FILING DATE: 2004-08-26
; PRIOR APPLICATION NUMBER: 60/489,238

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; PRIOR FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-927-634-63

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Query Match          56.8%; Score 21; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 VLXDDLE 8
       |||||
Db      1 ILDDWLE 8

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RESULT 5
US-11-129-143-168
; Sequence 168, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HOMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Bradyrhizobium japonicum
US-11-129-143-168

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Query Match          54.1%; Score 20; DB 7; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy      4 DDLLE 8
       |||||
Db      1 DDILD 5

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RESULT 6
US-11-129-143-169
; Sequence 169, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HOMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 169
; LENGTH: 5
; TYPE: PRT

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; ORGANISM: Rhizobium sp. strain NGR234
US-11-129-143-169

Query Match 54.1%; Score 20; DB 7; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8
||:|:
DB 1 DDILD 5

RESULT 7
US-11-129-143-170
; Sequence 170, Application US/11129143
; Publication No. US20050266518A1

; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-11-129-143-170

Query Match 54.1%; Score 20; DB 7; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8
||:|:
DB 1 DDILD 5

RESULT 8
US-11-129-143-171
; Sequence 171, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 171
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-11-129-143-171

Query Match 54.1%; Score 20; DB 7; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8
||:|:

DB 1 DDILD 5

RESULT 9
US-11-129-143-172
; Sequence 172, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.

; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-129-143-172

Query Match 54.1%; Score 20; DB 7; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8
||:|:
DB 1 DDILD 5

RESULT 10
US-11-129-143-173
; Sequence 173, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 173
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-11-129-143-173

Query Match 54.1%; Score 20; DB 7; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8
||:|:
DB 1 DDILD 5

RESULT 11
US-10-982-440-126
; Sequence 126, Application US/10982440
; Publication No. US20060018909A1
; GENERAL INFORMATION:
; APPLICANT: Oliner, John

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; APPLICANT: Graham, Kevin
; TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
; FILE REFERENCE: 04-881-A
; CURRENT APPLICATION NUMBER: US/10/982,440
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/620,161
; PRIOR FILING DATE: 2004-10-19
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 126
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-982-440-126

Query Match
Best Local Similarity 54.1%; Score 20; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 7
Db 2 DDL 5

RESULT 12
US-11-021-305-62
; Sequence 62, Application US/11021305
; Publication No. US20050282733A1
; GENERAL INFORMATION:
; APPLICANT: Prius, Johannes B
; APPLICANT: Hutley, Louise J
; TITLE OF INVENTION: Differentiation-modulating agents and uses therefor
; FILE REFERENCE: DAV1169.001CPI
; CURRENT APPLICATION NUMBER: US/11/021,305
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: USSN 60/392,130
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
; LENGTH: 8
; TYPE: PRT
; ORGANISM: mammalian
; US-11-021-305-62

Query Match
Best Local Similarity 54.1%; Score 20; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 7
Db 4 DDL 7

RESULT 13
US-11-021-305-65
; Sequence 65, Application US/11021305
; Publication No. US20050282733A1
; GENERAL INFORMATION:
; APPLICANT: Prius, Johannes B
; APPLICANT: Hutley, Louise J
; TITLE OF INVENTION: Differentiation-modulating agents and uses therefor
; FILE REFERENCE: DAV1169.001CPI
; CURRENT APPLICATION NUMBER: US/11/021,305
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: USSN 60/392,130
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 65
; LENGTH: 8
; TYPE: PRT
; ORGANISM: mammalian
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US-11-021-305-65

Query Match
Best Local Similarity 54.1%; Score 20; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 7
Db 4 DDL 7

RESULT 14
US-11-021-305-66
; Sequence 66, Application US/11021305
; Publication No. US20050282733A1
; GENERAL INFORMATION:
; APPLICANT: Prius, Johannes B
; APPLICANT: Hutley, Louise J
; TITLE OF INVENTION: Differentiation-modulating agents and uses therefor
; FILE REFERENCE: DAV1169.001CPI
; CURRENT APPLICATION NUMBER: US/11/021,305
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: USSN 60/392,130
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 66
; LENGTH: 8
; TYPE: PRT
; ORGANISM: mammalian
; US-11-021-305-66

Query Match
Best Local Similarity 54.1%; Score 20; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 7
Db 4 DDL 7

RESULT 15
US-11-207-078-373
; Sequence 373, Application US/11207078
; Publication No. US20060040307A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Langner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/207,078
; FILING DATE: 17-Aug-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,477
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FILING DATE: 22-NOV-2000
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 373:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 373:
US-11-207-078-373

Query Match 51.4%; Score 19; DB 7; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 LKDDL 7
| | | |
Db 1 LVDDFL 6

Search completed: April 6, 2006, 16:51:12
Job time : 13.3333 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:12:46 ; Search time 111.667 Seconds
(without alignments)
35.413 Million cell updates/sec

Title: US-10-791-217A-2

Perfect score: 45
Sequence: 1 VHHDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 401289

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Minimum DB seq length: 0
Maximum DB seq length: 9
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: genseq.1990s:*
3: genseq.2000s:*
4: genseq.2001s:*
5: genseq.2002s:*
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9: genseq.2005s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	45	100.0	2	AAW9196 Minor hist
2	45	100.0	2	AAW97375 HA-1 H-al
3	45	100.0	9	ADH40333 Human hist
4	37	82.2	2	AAW9197 Minor hist
5	37	82.2	2	AAW97374 HA-1 R-al
6	37	82.2	9	ADH40334 Human minor hist
7	36	80.0	2	AAW9195 Minor hist
8	36	80.0	2	AAW97572 T-cell ep
9	31	68.9	8	ADU93853 BC24 tumor
10	30	66.7	2	AAW97373 Peptide e
11	28	62.2	9	AAAY10122 T cell ep
12	28	62.2	9	ABG79805 MHC class
13	28	62.2	9	ADK68732 Epitope 1
14	28	62.2	9	ADK05291 Hepatitis
15	28	62.2	9	ADK05293 Hepatitis
16	28	62.2	9	ADQ10530 Cercopit
17	28	62.2	9	ADS81010 Tumour-as
18	27	60.0	9	ABJ20115 MHC bindi
19	27	60.0	8	ADT02787 Human tum
20	26	57.8	6	ABU97233 Enzyme pe
21	26	57.8	6	ABU97232 Enzyme pe
22	26	57.8	6	ABU97234 Enzyme pe
23	26	57.8	6	ABU97231 Enzyme pe
24	26	57.8	6	ADY63770 Human alb

25	26	57	8	7	8	AA096262	Human	ser	Adm96262
26	26	57	8	8	5	AA096262	Human	mag	Adm96262
27	26	57	8	9	8	ADM96261	Human	ser	Adm96261
28	26	57	8	9	8	ADM96258	Human	ser	Adm96258
29	26	57	8	9	8	ADT73023	Human	RSV	AdT73023
30	26	57	8	9	8	ADT49074	Human	BFA	AdT49074
31	26	57	8	9	8	ADU96636	BFA	tumo	AdU96636
32	25	55	6	6	6	ABU97229	Enzyme	pe	AbU97229
33	25	55	6	6	6	ABU97230	Enzyme	pe	AbU97230
34	25	55	6	9	4	AA079144	Amino	ter	AA079144
35	25	55	6	9	4	AB084492	Peptide	f	AB084492
36	25	55	6	9	5	AA026631	Year0	GPA	AA026631
37	25	55	6	9	7	AD025889	Year0	GPA	AD025889
38	24	53	3	6	2	AA029358	Endotheli		AA029358
39	24	53	3	6	2	AA069140	Endotheli		AA069140
40	24	53	3	7	2	AA063186	Altered	I	AA063186
41	24	53	3	7	4	AA070589	Human	imm	AA070589
42	24	53	3	7	5	AA021066	Isoeerie		AA021066
43	24	53	3	7	5	AA028095	Human	imm	AA028095
44	24	53	3	8	8	ADT39874	SARS	vir	AdT39874
45	24	53	3	8	8	AD078693	SARS	vir	Ad078693

ALIGNMENTS

RESULT 1
AAW99196
ID AAW99196 standard; peptide; 9 AA.
...

DT 20-MAY-1999 (first entry)

DE Minor histocompatibility antigen HA-1 T-cell epitope #2.

KM Minor histocompatibility antigen, HA-1; T-cell epitope; immunological,
KM graft versus host disease; bone marrow transplant; leukaemia; vaccine
KM diagnosis; aplastic anaemia; immune deficiency disease.

OS Homo sapiens.

PN W09905174-A1.

PD 04-FEB-1999.

PF 23-JUL-1998; 98WO-NL000425.

PR 23-JUL-1997; 97EP-00202303.

PA (UYLE-) RIJKSUNIV LEIDEN.

PI Goulimy EAJM, Hunt DF, Engelhard VH;

DR WPI; 1999-153312/13.

PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.

PS Claim 3; Page 32; 47pp; English.

CC The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host diseases, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases

SQ Sequence 9 AA:

50

```

Query Match          100.0%; Score 45; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VLHDDLLEA 9
    |||||
Db 1 VLHDDLLEA 9

RESULT 2
AAW97375
ID AAW97375 standard; protein; 9 AA.
AC AAW97375;
XX
XX
XX 13-MAY-1999 (first entry)
XX
XX HA-1-H-allele sequence.
XX
XX Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
XX R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
XX severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
XX
XX Homo sapiens.
XX
XX MO9905313-A2.
XX
XX 04-FEB-1999.
XX
XX 23-JUL-1998; 98WO-EP004928.
XX
XX 23-JUL-1997; 97EP-00202303.
XX
XX 02-JUN-1998; 98EP-00870125.
XX
XX (UYLE-) RUCKSUNIV LEIDEN.
XX
XX Goumy E;
XX
XX WPI; 1999-142960/12.
XX
XX Typing minor histocompatibility antigen HA-1 - by amplifying and
XX identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
XX of genetic aberrances.
XX
XX Claim 18; Fig 5; 59pp; English.
XX
XX The present sequence represents part of the minor histocompatibility
XX antigen HA-1 H-allele. The specification describes methods for typing
XX alleles (preferably the H and R alleles) of the minor histocompatibility
XX antigen HA-1 in a sample, which comprise detecting polymorphic
XX nucleotides in the cDNA or genomic nucleic acids of the alleles. The
XX methods can be used for HA-1 typing for bone marrow transplants, severe
XX aplastic anaemia, leukaemia and immune deficiency diseases, as well as
XX detection of genetic aberrances. The probes and primers of the invention
XX can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
XX anti-idiotypic B cells and/or T cells and antibodies
XX
XX Sequence 9 AA;
XX
XX Query Match          100.0%; Score 45; DB 2; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Oy 1 VLHDDLLEA 9
XX    |||||
XX Db 1 VLHDDLLEA 9
XX
XX RESULT 3
XX ADH40333
XX ID ADH40333 standard; peptide; 9 AA.
XX
XX AC ADH40333;

```

```

XX
XX 11-MAR-2004 (first entry)
XX
XX Human minor histocompatibility antigen HA-1 T cell epitope.
XX
XX human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
XX minor histocompatibility antigen; mAb; T cell epitope.
XX
XX Homo sapiens.
XX
XX WO2003106692-A2.
XX
XX 24-DEC-2003.
XX
XX 13-JUN-2003; 2003WO-EP006251.
XX
XX 13-JUN-2002; 2002EP-00013423.
XX
XX (MERE ) MERCK PATENT GMBH.
XX
XX Strltmacter W, Mo11 H;
XX
XX WPI; 2004-082200/08.
XX
XX Providing allelic variant epitope of protein based on single nucleotide
XX polymorphism by defining target protein, screening database of protein,
XX identifying, selecting allelic variant protein, creating variant
XX epitopes.
XX
XX Disclosure; Page 82; 119pp; English.
XX
XX The invention relates to a novel method for providing epitopes of allelic
XX variants of antigenic proteins from specific species based on single
XX nucleotide polymorphism (SNP), by defining target protein/peptide or its
XX subset, screening database or DNA encoding target protein, identifying,
XX selecting allelic peptide/protein variants, expression product or its
XX fragment encoded by DNA sequence having SNP, creating variant epitopes,
XX selecting epitopes binding to MHC protein. A protein of the invention has
XX cytostatic activity, and may have a use in a vaccine. The method is
XX useful for generating a SNP profile of one or more individuals from a
XX given species by applying the method for several protein from the
XX individuals, where the SNP profile was related to disease, preferably
XX cancer. This is useful for diagnosing a disease in an individual by
XX generating the SNP-related polymorphic profile. A method of the invention
XX is useful for transplanting haematopoietic stem cells from a donor to a
XX recipient and treating cancer, preferably leukemia, and for determining
XX the progression, regression or onset of a treated disease. The present
XX sequence is used in the exemplification of the invention.
XX
XX Sequence 9 AA;
XX
XX Query Match          100.0%; Score 45; DB 8; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Oy 1 VLHDDLLEA 9
XX    |||||
XX Db 1 VLHDDLLEA 9
XX
XX RESULT 4
XX AAW99197
XX ID AAW99197 standard; peptide; 9 AA.
XX
XX AC AAW99197;
XX
XX 20-MAY-1999 (first entry)
XX
XX Minor histocompatibility antigen HA-1 T-cell epitope #3.
XX
XX Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
XX graft versus host disease; bone marrow transplant; leukaemia; vaccine;
XX diagnosis; aplastic anaemia; immune deficiency disease.
XX
XX

```

XX Homo sapiens.
 OS
 XX WO9905174-A1.
 PN
 XX 04-FEB-1999.
 PD
 XX 23-JUL-1998; 98WO-NL000425.
 PF
 XX 23-JUL-1997; 97EP-00202303.
 PR
 XX (UYLE-) RIJXSUNIV LEIDEN.
 PA
 XX Goulmy EAJM, Hunt DF, Engelhard VH;
 PI
 XX WPI; 1999-153312/13.
 DR
 XX A new minor histocompatibility antigen, HA-1 - useful to treat immune
 PT diseases and prevent rejection and host versus graft disease in bone
 PR marrow and organ transplantation.
 PS
 XX Disclosure; Page 15; 47pp; English.
 CC
 XX The present sequence represents a new peptide (P1) constituting a T-cell
 CC epitope obtainable from the minor histocompatibility antigen HA-1. The
 CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
 CC as a medicine, to induce tolerance for transplants, prevent rejection
 CC and/or graft versus host disease, or to treat (auto) immune diseases. In
 CC particular it can be used with bone marrow transplantation, in the
 CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
 CC diseases
 CC
 XX
 SQ Sequence 9 AA;

Query Match 82.2%; Score 37; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLTA 9
 Db 1 VLHDDLTA 9

RESULT 5
 AAM97374
 ID AAM97374 standard; protein; 9 AA.
 XX
 AC AAM97374;
 XX
 DT 13-MAY-1999 (first entry)
 XX
 DB HA-1 R-allele sequence.
 XX
 KW Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
 KW R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
 KW severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9905174-A2.
 XX
 PD 04-FEB-1999.
 XX
 PF 23-JUL-1998; 98WO-EP004928.
 XX
 PR 23-JUL-1997; 97EP-00202303.
 PR 02-JUN-1998; 98EP-00870125.
 XX
 PA (UYLE-) RIJXSUNIV LEIDEN.
 XX
 PI Goulmy E;
 XX
 DR WPI; 1999-142960/12.

XX Typing minor histocompatibility antigen HA-1 - by amplifying and
 PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
 PT of genetic aberrances.
 XX
 XX Claim 13; Fig 5; 59pp; English.

XX The present sequence represents part of the minor histocompatibility
 CC antigen HA-1 R-allele. The specification describes methods for typing
 CC alleles (preferably the H and R alleles) of the minor histocompatibility
 CC antigen HA-1 in a sample, which comprise detecting polymorphic
 CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
 CC methods can be used for HA-1 typing for bone marrow transplants, severe
 CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
 CC detection of genetic aberrances. The probes and primers of the invention
 CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
 CC anti-idiotypic B cells and/or T cells and antibodies

SQ Sequence 9 AA;

Query Match 82.2%; Score 37; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLTA 9
 Db 1 VLHDDLTA 9

RESULT 6
 ADH40334
 ID ADH40334 standard; peptide; 9 AA.
 XX
 AC ADH40334;
 XX
 DT 11-MAR-2004 (first entry)

DE Human minor histocompatibility antigen HA-1 T cell epitope.

XX human; cytostatic; vaccine; SNP profile; cancer; leukaemia;

KW minor histocompatibility antigen; mHAg; T cell epitope.

XX

OS Homo sapiens.

PN WO2003106692-A2.

PD 24-DEC-2003.

PF 13-JUN-2003; 2003WO-EP006251.

PR 13-JUN-2002; 2002EP-00013423.

PA (MERE) MERCK PATENT GMBH.

PI Strittmatter W, Moll H;

DR WPI; 2004-082200/08.

XX Providing allelic variant epitope of protein based on single nucleotide
 PT polymorphism by defining target protein, screening database of protein,
 PT identifying, selecting allelic variant protein, creating variant
 PT epitopes.

PS Disclosure; Page 82; 119pp; English.

XX The invention relates to a novel method for providing epitopes of allelic
 CC variants of antigenic proteins from specific species based on single
 CC nucleotide polymorphism (SNP), by defining target protein/peptide or its
 CC subset, screening database of DNA encoding target protein, identifying,
 CC selecting allelic peptide/protein variants, expression product or its
 CC fragment encoded by DNA sequence having SNP, creating variant epitopes,
 CC selecting epitopes binding to MHC protein. A protein of the invention has
 CC cytostatic activity, and may have a use in a vaccine. The method is

CC useful for generating a SNP profile of one or more individuals from a
 CC given species by applying the method for several protein from the
 CC individuals, where the SNP profile was related to disease, preferably
 CC cancer. This is useful for diagnosing a disease in an individual by
 CC generating the SNP-related polymorphic profile. A method of the invention
 CC is useful for transplanting haematopoietic stem cells from a donor to a
 CC recipient and treating cancer, preferably leukaemia, and for determining
 CC the progression, regression or onset of a treated disease. The present
 CC sequence is used in the exemplification of the invention.

CC Sequence 9 AA;

Query Match 82.2%; Score 37; DB 8; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 VLHDDLLEA 9
 |||||
 1 VLKDDLLEA 9

RESULT 7
 AAW9195
 ID AAW9195 standard; peptide; 9 AA.
 AC AAW9195;

DT 20-MAY-1999 (first entry)

DE Minor histocompatibility antigen HA-1 T-cell epitope #1.

KM Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
 KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
 diagnosis; aplastic anaemia; immune deficiency disease.

OS Homo sapiens.
 OS Synthetic.

FH Key Location/Qualifiers
 FT Misc-difference 3 /label= His, Arg
 XX

PN WO9905174-A1.

PD 04-FEB-1999.

PF 23-JUL-1998; 98WO-NL000425.

PR 23-JUL-1997; 97EP-00202303.

PA (UYLE-) RIJKSUNIV LEIDEN.

PI Goulmy EAJM, Hunt DF, Engelhard VH;

DR WPI; 1999-153312/13.

PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
 PT diseases and prevent rejection and host versus graft disease in bone
 PT marrow and organ transplantation.

PS Claim 1; Page 32; 47pp; English.

CC The present sequence represents a new peptide (P1) constituting a T-cell
 CC epitope obtainable from the minor histocompatibility antigen HA-1. The
 CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
 CC as a medicine, to induce tolerance for transplants, prevent rejection
 CC and/or graft versus host disease, or to treat (auto) immune diseases. In
 CC particular it can be used with bone marrow transplantation, in the
 CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
 CC diseases

XX Sequence 9 AA;

Query Match 80.0%; Score 36; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 VLHDDLLEA 9
 |||||
 1 VLKDDLLEA 9

RESULT 8
 AAW91572
 ID AAW91572 standard; peptide; 9 AA.
 AC AAW91572;

DT 20-MAY-1999 (first entry)

DE T-cell epitope from the minor histocompatibility antigen HA-1.

KM T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
 KW transplant rejection; Graft-versus-Host Disease; autoimmune disease;
 KM neoplastic haematopoietic cell.

OS Homo sapiens.

FH Key Location/Qualifiers
 FT Misc-difference 3 /note= "His or Arg"
 FT

PN WO9905173-A1.

PD 04-FEB-1999.

PF 23-JUL-1998; 98WO-NL000424.

PR 23-JUL-1997; 97EP-00202303.

PA (UYLE-) RIJKSUNIV LEIDEN.

PI Goulmy EAJM, Hunt DF, Engelhard VH;

DR WPI; 1999-142855/12.

PT Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
 PT for inducing tolerance to transplants and prevent rejection or graft-
 PT versus-host disease.

PS Claim 1; Page 39; 57pp; English.

CC The present sequence represents an immunogenic peptide constituting a T-
 CC cell epitope, obtainable from the minor histocompatibility antigen HA-1.
 CC The peptide can be used in vaccines or pharmaceutical formulations as
 CC medicines to induce tolerance for transplants so as to prevent rejection
 CC and/or Graft-versus-Host Disease, or to treat autoimmune diseases.
 CC Neoplastic haematopoietic cells presenting the peptides, in an HLA class
 CC I context, can be eliminated after specific recognition of the peptides.
 CC The peptides can also be used to raise antibodies, T-cell receptor, B-
 CC and T-cells

XX Sequence 9 AA;

Query Match 80.0%; Score 36; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 VLHDDLLEA 9
 |||||
 1 VLKDDLLEA 9

RESULT 9
 ADU99853
 ID ADU99853 standard; peptide; 9 AA.


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XX AC ADU99853;
XX XX 24-FEB-2005 (first entry)
XX DT BC24 tumor antigen antigenic peptide #85.
XX DE expression vector; tumor antigen; cancer; cytostatic; BC24;
XX KW antigenic peptide.
XX OS Unidentified.
XX PN WO2004104039-A2.
XX PD 02-DEC-2004.
XX PF 15-MAY-2004; 2004WO-US015202.
XX PR 16-MAY-2003; 2003US-0471119P.
XX PR 16-MAY-2003; 2003US-0471193P.
XX PA (AVERT ) AVENTIS PASTEUR INC.
XX PI Berinstein N, Gallichan S, Lovitt C, Farrington M, Radvanyi L;
XX PI Singh-Sandhu D;
XX DR WPI; 2004-834272/82.
XX XX
XX PT New expression vector comprising a nucleic acid encoding a tumor antigen,
XX PT e.g. BFA4, BCY1, BFA5, BC24, or BFA3, useful for expressing multiple
XX PT tumor antigens, or for preventing or treating cancer.
XX PS Example 8; Page 60; 109pp; English.
XX CC The invention comprises an expression vector that contains a nucleic acid
XX CC encoding a tumor antigen (e.g. BC24 or BFA3). The expression vector of
XX CC the invention is useful for the expression of multiple tumor antigens and
XX CC the prevention or treatment of cancer. The present amino acid sequence
XX CC represents a BC24 tumor antigen antigenic peptide that was used in an
XX CC example of the invention.
XX SQ Sequence 9 AA;

Query Match 68.9%; Score 31; DB 8; Length 9;
Best Local Similarity 85.7%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 1;

QY 2 LHDDLLLE 8
Db 2 LHSDLLLE 8

RESULT 10
AAW97373
ID AAW97373 standard; peptide; 9 AA.
XX AC AAW97373;
XX DT 13-MAY-1999 (first entry)
XX DE Peptide epitope of HA-1 antigen.
XX KW Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
XX KW R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
XX KW severe aplastic anaemia; leukaemia; immune deficiency disease.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 2 /note= "not specified"
XX FT Misc-difference 6 /note= "not specified"
XX FT

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FT FT Misc-difference 7 /note= "not specified"
XX FT
XX PN WO9905313-A2.
XX PD 04-FEB-1999.
XX PF 23-JUL-1998; 98WO-BP004928.
XX PR 23-JUL-1997; 97EP-00202303.
XX PR 02-JUN-1998; 98EP-00870125.
XX PA (UYLE-) RIJKSUNIV LEIDEN.
XX PI Goulmy E;
XX DR WPI; 1999-142960/12.
XX XX
XX PT Typing minor histocompatibility antigen HA-1 - by amplifying and
XX PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
XX PT of genetic aberrances.
XX PS Example 1; Page 22; 59pp; English.
XX CC The present sequence represents an epitope of the minor
XX CC histocompatibility antigen HA-1. The specification describes methods for
XX CC typing alleles (preferably the H and R alleles) of the minor
XX CC histocompatibility antigen HA-1 in a sample, which comprise detecting
XX CC polymorphic nucleotides in the cDNA or genomic nucleic acids of the
XX CC alleles. The methods can be used for HA-1 typing for bone marrow
XX CC transplants, severe aplastic anaemia, leukaemia and immune deficiency
XX CC diseases, as well as detection of genetic aberrances. The probes and
XX CC primers of the invention can be used to screen for the HA-1 alleles. The
XX CC HA-1 peptides can be used anti-idiotypic B cells and/or T cells and
XX CC antibodies.
XX SQ Sequence 9 AA;

Query Match 66.7%; Score 30; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2e+06; 3; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 3;

QY 1 VTHDDLLLEA 9
Db 1 VXHDDXXEA 9

RESULT 11
AAV10122
ID AAV10122 standard; peptide; 9 AA.
XX AC AAV10122;
XX DT 12-MAY-1999 (first entry)
XX DE T cell epitope/MHC ligand SEQ ID NO:52.
XX KW Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;
XX KW immunisation; tumour; infectious disease; immunotherapy; cancer;
XX KW malignant melanoma; viral disease; hepatitis; AIDS.
XX OS Synthetic.
XX OS Human herpesvirus 4.
XX PN WO9902183-A2.
XX PD 21-JAN-1999.
XX PF 10-JUL-1998; 98WO-US014289.
XX PR 10-JUL-1997; 97CA-02209815.
XX PR 10-DEC-1997; 97US-00988320.
XX

```


XX This invention relates to a novel method of identifying a polypeptide
CC suitable for epitope liberation, including the steps of identifying an
CC epitope of interest; providing substrate polypeptide sequence including
CC the epitope, wherein the substrate permits processing by a proteasome;
CC contacting the substrate with a composition including the proteasome,
CC under conditions that support processing of the substrate by proteasome;
CC and assaying for liberation of epitope. The invention may be useful for
CC the development of compounds with a cytostatic, antibacterial,
CC prozoacidal or fungicidal activity acting as T-cell activators. In
CC addition, the invention may allow development of a vaccine. The invention
CC is useful for identifying a polypeptide suitable for epitope liberation,
CC where the epitope is a housekeeping epitope. The compositions comprising
CC the identified housekeeping epitopes are useful in vitro in vaccine
CC development or in the generation or expansion of cytotoxic T lymphocyte
CC (CTL) to be used in adoptive immunotherapy. The invention is also useful
CC for activating T-cells against neoplastic cells, and cells infected with
CC virus, bacterium, protozoan or fungus. CTL epitopes are identified based
CC on the knowledge that such epitopes are, in fact, produced by the
CC housekeeping proteasome system. Once identified, these epitopes, embodied
CC as peptides, can be used to successfully immunise or induce therapeutic
CC CTL responses against housekeeping proteasome expressing target cells in
CC the host. The present sequence is that of a peptide which is related to
CC the method of the invention.

SQ Sequence 9 AA;

Query Match 62.2%; Score 28; DB 8; Length 9;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHDDL 6
|||:
4 VHDDL 9

Db

RESULT 14
ADK05291

ADK05291 standard; peptide; 9 AA.
ADK05291;
06-MAY-2004 (first entry)

DE Hepatitis C virus CTL epitope peptide #3121.

KM pathogenic virus; alternative reading frame; antigenic determinant;
KM virucide; vaccine; therapeutic agent; infection; epitope peptide;
KM HLA-allele; CTL.

XX Hepatitis C virus.

XX WO2004011650-A2.

XX 05-FEB-2004.

XX 24-JUL-2003; 2003WO-EP008112.

XX 24-JUL-2002; 2002AT-00001124.

XX 11-JUL-2003; 2003EP-00450171.

XX (INTE-) INTERCELL AG.

XX Mattner F, Schmidt W, Habel A;

XX MPI, 2004-169243/16.

PT New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
PT preventing an infection with the pathogenic virus.

PS Claim 14; Page 114; 220pp; English.

CC This invention relates to a novel polypeptide encoded by an alternative
CC reading frame of a pathogenic virus, where the polypeptide starts with a
CC methionine amino acid residue, which comprises an antigenic determinant
CC and more than 7 amino acid residues. The invention may be useful for the
CC production of compounds with a virucide activity or the development of a
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC agent. It is also useful for the manufacture of a medicament for treating
CC or preventing an infection with the pathogenic virus. The present
CC sequence is that of a hepatitis C virus CTL epitope peptide of the
CC invention.

SQ Sequence 9 AA;

Query Match 62.2%; Score 28; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDDLL 7
|||:
4 HDDLL 8

Db

RESULT 15
ADK05293

ADK05293 standard; peptide; 9 AA.

ADK05293;

06-MAY-2004 (first entry)

DE Hepatitis C virus CTL epitope peptide #3123.

KM pathogenic virus; alternative reading frame; antigenic determinant;
KM virucide; vaccine; therapeutic agent; infection; epitope peptide;
KM HLA-allele; CTL.

XX Hepatitis C virus.

XX WO2004011650-A2.

XX 05-FEB-2004.

XX 24-JUL-2003; 2003WO-EP008112.

XX 24-JUL-2002; 2002AT-00001124.

XX 11-JUL-2003; 2003EP-00450171.

XX (INTE-) INTERCELL AG.

XX Mattner F, Schmidt W, Habel A;

XX MPI, 2004-169243/16.

PT New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
PT preventing an infection with the pathogenic virus.

PS Claim 14; Page 114; 220pp; English.

CC This invention relates to a novel polypeptide encoded by an alternative
CC reading frame of a pathogenic virus, where the polypeptide starts with a
CC methionine amino acid residue, which comprises an antigenic determinant
CC and more than 7 amino acid residues. The invention may be useful for the
CC production of compounds with a virucide activity or the development of a
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC agent. It is also useful for the manufacture of a medicament for treating
CC or preventing an infection with the pathogenic virus. The present
CC sequence is that of a hepatitis C virus CTL epitope peptide of the
CC invention.

SQ Sequence 9 AA;

Query Match 62.2%; Score 28; DB 8; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HDDLL 7
|||
Db 4 HDDLL 8

Search completed: April 6, 2006, 16:19:13
Job time : 114.667 secs

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: April 6, 2006, 16:19:36 ; Search time 18.6667 Seconds
(without alignments)
46.380 Million cell updates/sec

Title: US-10-791-217a-2

Perfect score: 45

Sequence: 1 VILHDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	40.0	7	2	I46868
2	17	37.8	7	2	S55696
3	16	35.6	7	2	PQ0663
4	16	35.6	7	2	S68004
5	16	35.6	8	2	PC4131
6	15	33.3	6	2	S78764
7	15	33.3	7	2	A59489
8	14	31.1	7	2	S20446
9	14	31.1	8	2	XGHUEU
10	14	31.1	9	2	A12872
11	14	31.1	9	2	S10920
12	14	31.1	9	2	A60427
13	13	28.9	8	2	A61328
14	13	28.9	9	2	PH0342
15	12	26.7	4	2	I40697
16	12	26.7	5	2	PT0679
17	12	26.7	5	2	PT0601
18	12	26.7	6	2	B35640
19	12	26.7	6	2	PT0533
20	12	26.7	7	2	A34026
21	12	26.7	7	2	B39040
22	12	26.7	7	2	PT0628
23	12	26.7	7	2	PT0722
24	12	26.7	7	2	PT0576
25	12	26.7	8	2	PT0368
26	12	26.7	8	2	PN0043
27	12	26.7	8	2	PT0557
28	12	26.7	9	2	A60108
29	12	26.7	9	2	PM0002

30	12	26.7	9	2	S65913	pyrimidine syntheses
31	12	26.7	9	2	PH0108	late Gl-69 protein
32	12	26.7	9	2	PT0562	T-cell receptor be
33	12	26.7	9	2	B30572	T-cell receptor be
34	11	24.4	5	2	C41225	copper resistance
35	11	24.4	5	2	T10954	hypothetical prote
36	11	24.4	6	2	T11779	phosphoglycerate t
37	11	24.4	7	2	S25266	p1le protein - Esc
38	11	24.4	7	2	PT0246	Ig heavy chain CRD
39	11	24.4	8	2	S22428	chitin-binding pro
40	11	24.4	8	2	B33099	158k exoantigen -
41	11	24.4	8	2	S69165	ferredoxin a2 - Ja
42	11	24.4	9	2	S66419	tetrameric protein
43	11	24.4	9	2	PT0272	Ig heavy chain CRD
44	11	24.4	9	2	A11497	transaldolase (EC
45	11	24.4	9	2	B39504	octamer-binding pr

ALIGNMENTS

RESULT 1
I46868
alpha-myosin heavy chain - rabbit (fragment)
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C/Accession: I46868
R/Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.
Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984
A/Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricul
A/Reference number: I46868, MID:84221901, PMID:6328491
A/Accession: I46868
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-7 <FRI>
A/Cross-references: UNIPROT:Q28742; UNIPARC:UPI0000087938; GB:X01698; MID:g165538; PIDN

Query Match
Best Local Similarity 40.0%; Score 18; DB 2; Length 7;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LKDD 5
DB 3 MKDE 6

RESULT 2
S55696
phosphoenolpyruvate carboxylase - Trypanosoma brucei
C/Species: Trypanosoma brucei
C/Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C/Accession: S55696
R/Hunt, M.; Koehler, P.
Biochim. Biophys. Acta 1249, 15-22, 1995
A/Title: Purification and characterization of phosphoenolpyruvate carboxylase from Tr
A/Reference number: S55696; MID:95284106; PMID:776679
A/Accession: S55696
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <HUN>
A/Cross-references: UNIPROT:Q7M355; UNIPARC:UPI000017B599

Query Match
Best Local Similarity 37.8%; Score 17; DB 2; Length 9;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VILHDDL 6
DB 3 ITHKNVL 8

RESULT 3
PQ0663

membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment)
C:Species: porcine epidemic diarrhea virus
C>Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 08-Oct-1999
C:Accession: PQ0663
R:Brigden, A.; Duarte, M.; Tobler, K.; Laude, H.; Ackermann, M.
J. Gen. Virol. 74, 1795-1804, 1993
A:Title: Sequence determination of the nucleocapsid protein gene of the porcine epidemic
isolate gastroenteritis virus.
A:Reference number: UQ2191; MUID:93389433; PMID:8397280
A:Accession: PQ0663
A:Molecule type: mRNA
A:Residues: 1-7 <BRI>
A:Cross-references: UNIPARC:UPI0000170FAC; GB:Z14976; NID:G311650; P1DN:CAA78699.1; PID:
C:Comment: This virus is coronavirus related to human coronavirus 229E.
C:Keywords: membrane protein

Query Match
Best Local Similarity 100.0%; Score 16; DB 2; Length 7;
Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLN 3
|||
Db 3 VLN 5

RESULT 4
S68004
hucolin, 75K chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S68004
R:Edgar, P.F.
FEBS Lett. 375, 159-161, 1995
A:Title: Hucolin, a new corticosteroid-binding protein from human plasma with structural
A:Reference number: S68004; MUID:96087107; PMID:7498469
A:Accession: S68004
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <BDG>
A:Cross-references: UNIPARC:UPI000017C164

Query Match
Best Local Similarity 100.0%; Score 16; DB 2; Length 7;
Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DDL 6
|||
Db 4 DDL 6

RESULT 5
PC4131
hypothetical protein 8 [imported] - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004
C:Accession: PC4131
R:Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.
Gene 167, 87-91, 1995
A:Title: Sequencing and characterization of the downstream region of the genes encoding
Y for biosynthesis of heme d1.
A:Reference number: JG4552; MUID:96144254; PMID:8566817
A:Accession: PC4131
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <KMW>
A:Cross-references: UNIPROT:P95412; UNIPARC:UPI000017A96A; DDBJ:DS0473; NID:G1217594
A:Note: this ORF is not annotated in GenBank entry PSENIRC, release 113.0
C:Superfamily: Pseudomonas stutzeri nrid protein

Query Match
Best Local Similarity 100.0%; Score 16; DB 2; Length 8;
Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DDL 6
|||
Db 2 DDL 4

RESULT 6
S78764
ribosomal protein MRP-S23, mitochondrial - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: S78764
R:Grack, H.R.
Submitted to the Protein Sequence Database, July 1999
A:Reference number: S78760
A:Accession: S78764
A:Molecule type: protein
A:Residues: 1-6 <GRA>
A:Cross-references: UNIPARC:UPI000017C570
C:Keywords: mitochondrion
P/1-6/Product: ribosomal protein MRP-S23 (fragment) #status experimental <MAT>

Query Match
Best Local Similarity 75.0%; Score 15; DB 2; Length 6;
Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 LHDD 5
|||
Db 1 LHVD 4

RESULT 7
A59489
protein kinase C inhibitor - rat (fragment)
C:Species: Rattus norvegicus
C>Date: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 25-Aug-2003
C:Accession: A59489
R:Negoro, M.
Submitted to the Protein Sequence Database, June 2003
A:Description: Purification of PKCI from rat liver.
A:Reference number: A59489
A:Accession: A59489
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <NEG>
A:Experimental source: strain Wistar, liver
A:Note: p-Hydroxyacetophenone-Sephacrose binding protein

Query Match
Best Local Similarity 40.0%; Score 15; DB 2; Length 7;
Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VLHDD 5
: |||
Db 2 IFHDD 6

RESULT 8
S20446
elastase - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C>Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
C:Accession: S20446
R:Kessler, E.; Saffrin, M.; Beretz, M.; Bursstein, Y.
FEBS Lett. 299, 291-293, 1992
A:Title: Identification of cleavage sites involved in proteolytic processing of Pseudom
A:Reference number: S20446; MUID:92183956; PMID:1544509
A:Accession: S20446
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <KES>
A:Cross-references: UNIPARC:UPI000017A95F

Query Match
Best Local Similarity 31.1%; Score 14; DB 2; Length 7;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 DLE 8
| | |
Db 3 DLD 6

RESULT 9

XGHUEU

urine glycopeptide - human

C/Species: Homo sapiens (man)

C/Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 16-Aug-2004

C/Accession: A03188

R/Lote, C.J.; Weiss, J.B.

Biochem. J. 123, 25P, 1971

A/Title: Identification in urine of a low-molecular-weight polar glycopeptide containing

A/Reference number: A03188; MUID:72062338; PMID:5126885

C/Accession: A03188

A/Molecule type: protein

A/Residues: 1-8 <LOT>

A/Cross-references: UNIPROT:P02729; UNIPARC:UPI000012849

C/Comment: The identity of the glycoprotein from which this peptide is derived is unknown

C/Keywords: glycoprotein

F1/Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match 31.1%; Score 14; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HD 4
| |
Db 5 HD 6

RESULT 10

A12872

transaldolase (EC 2.2.1.2) I - Yeast (*Pichia jadinii*) (fragment)C/Species: *Pichia jadinii*, *Candida utilis*

C/Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004

C/Accession: A12872

R/Sun, S.C.; Joris, L.; Tsolaie, O.

Arch. Biochem. Biophys. 178, 69-78, 1977

A/Title: Purification and crystallization of transaldolase isozyme I and evidence for di

A/Reference number: A12872; MUID:77110646; PMID:556924

C/Accession: A12872

A/Molecule type: protein

A/Residues: 1-9 <STUN>

A/Cross-references: UNIPROT:P17440; UNIPARC:UPI0000136884

C/Keyword: transferase

Query Match 31.1%; Score 14; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LHDDL 7
| | |
Db 3 IHCBTL 8

RESULT 11

S10920

venom protein HR-3 - oriental hornet (fragment)

C/Species: *Vespa orientalis* (oriental hornet)

C/Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004

C/Accession: S10920

R/Tulchibaev, M.U.; Akhmedova, N.U.; Karakov, I.; Korneev, A.S.; Gagel'gans, A.I.

Biochemistry (N.Y.) 53, 183-190, 1988

A/Title: Low-molecular-weight peptides of venom of the giant hornet *Vespa orientalis*. St

A/Reference number: S06445

C/Accession: S10920

A/Molecule type: protein

A/Residues: 1-9 <TUI>
A/Cross-references: UNIPROT:Q7M471; UNIPARC:UPI000017BF07
C/Keywords: venom

Query Match 31.1%; Score 14; DB 2; Length 9;
Best Local Similarity 28.6%; Pred. No. 2.8e+05;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 LHDDL 8
| | |
Db 3 VHEPLVK 9

RESULT 12

A60427

macrophage cytotoxicity-inducing factor, 29K - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004

C/Accession: A60427

R/Jones, C.M.; Prince, C.A.; Williams, J.S.

Exp. Hematol. 19, 704-709, 1991

A/Title: Purification and amino acid analysis of a human macrophage cytotoxicity-induc

A/Reference number: A60427; MUID:91372335; PMID:1909970

C/Accession: A60427

A/Molecule type: protein

A/Residues: 1-9 <TON>

A/Cross-references: UNIPROT:Q7M485; UNIPARC:UPI0000142BEO

A/Note: the sequence from the text on page 706 is inconsistent with that from page 708

C/Keywords: cytokine

Query Match 31.1%; Score 14; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLMD 4
| | |
Db 4 VLMD 7

RESULT 13

A61328

trypsin (EC 3.4.21.4) precursor - minke whale (fragment)

C/Species: *Balaenoptera acutorostrata* (minke whale, lesser rorqual)

C/Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004

C/Accession: A61328

R/Bricteux-Gregoire, S.; Schyns, R.; Floirkin, M.; Emmens, M.; Welling, G.W.; Beintema,

Biochim. Biophys. Acta 386, 244-255, 1975

A/Title: N-terminal amino acid sequence of trypsinogen from the lesser rorqual, *Balaen*

creas.

A/Reference number: A61328; MUID:75146765; PMID:1125273

C/Accession: A61328

A/Molecule type: protein

A/Residues: 1-8 <BRI>

A/Cross-references: UNIPROT:Q7M390; UNIPARC:UPI000017C43P

C/Keywords: hydrolase; protein digestion; serine proteinase; zymogen

F1-8/Domain: activation peptide #status experimental <APT>

Query Match 28.9%; Score 13; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LHDD 5
| | |
Db 3 IDDD 6

RESULT 14

PH0942

T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)

C/Species: *Rattus norvegicus* (Norway rat)

C/Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C/Accession: PH0942

R/Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991
A>Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0942
A:Molecule type: mRNA
A:Residues: 1-9 <GOL>
A:Cross-references: UNIPARC:UPI000017C9DD
A:Experimental source: complete Freund's adjuvant-immunized lymph node
A>Note: the authors translated the codon TGC for residue 2 as Ala
C:Keywords: T-cell receptor

Query Match 28.9%; Score 13; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LLE 8
|||
Db 5 LLE 7

RESULT 15

140697 biotin A - Citrobacter freundii (fragment)
C:Species: Citrobacter freundii
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: 140697
R:Shuan, D.; Campbell, A.
Gene 67, 203-211, 1988
A>Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter
A:Reference number: 140697; MUID:89006280; PMID:2971595
A:Accession: 140697
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 14 <RES>
A:Cross-references: UNIPROT:P13071; UNIPARC:UPI000017AA21; GB:M21922; NID:G144434

Query Match 26.7%; Score 12; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 5
|||
Db 3 DD 4

Search completed: April 6, 2006, 16:26:11
Job time : 19.6667 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 6, 2006, 16:13:46 ; Search time 118 Seconds

(without alignments)
53.611 Million cell updates/sec

Title: US-10-791-217A-2

Perfect score: 45

Sequence: 1 VLAHDLLEA 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 1766

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-Processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	42.2	9	2	Q7R8X5_PLAYO
2	19	42.2	9	2	Q47556_ECOLI
3	18	40.0	7	2	Q28742_RABIT
4	17	37.8	9	2	Q7M3S5_TRYP
5	16	35.6	7	2	Q99182_GSMG
6	16	35.6	8	2	Q7Z6G0_HUMAN
7	16	35.6	9	1	FAR8_MACRS
8	16	35.6	9	2	Q708W2_HUMAN
9	16	35.6	9	2	Q4X981_PLACH
10	16	35.6	9	2	Q8LPT5_MAIZE
11	15	33.3	9	2	P82568_STRPY
12	15	33.3	8	2	Q15900_HUMAN
13	15	33.3	8	2	Q4XK27_PLACH
14	15	33.3	9	2	Q9XJN0_GVIRU
15	15	33.3	6	1	TRP1_PBBPU
16	14	31.1	8	1	GLUR_HUMAN
17	14	31.1	8	2	Q9BFA7_MACPR
18	14	31.1	8	2	P72279_RHOGO
19	14	31.1	8	2	Q93SR0_STRAP
20	14	31.1	9	1	TALI_PTCUA
21	14	31.1	9	2	Q7M4R5_HUMAN
22	14	31.1	9	2	Q7M471_VESOR
23	14	31.1	9	2	Q9FSZ2_CICAR
24	14	31.1	9	2	Q8CG39_RAT
25	14	31.1	9	2	Q9QZAB_MOUSE
26	14	31.1	9	2	Q6Q7G0_RABRI
27	14	31.1	9	2	Q85710_RRTR
28	14	31.1	9	2	Q8UTD7_9HIV1
29	13	28.9	7	2	Q66205_9COCO
30	13	28.9	8	2	Q9HDS4_ASPFL
31	13	28.9	8	2	Q15889_HUMAN

32	13	28.9	8	2	Q7M390_BALAC	Q7M390 balaeopter
33	13	28.9	8	2	Q37854_BPR17	Q37854 bacterioph
34	13	28.9	8	2	Q6UC68_SORBN	Q6UC68 glycine max
35	13	28.9	8	2	Q7XB03_MAIZE	Q7XB03 zea mays (m
36	13	28.9	8	2	Q51594_9222Z	Q51594 plasmid col
37	13	28.9	9	2	Q6UVK2_MALDO	Q6UVK2 malus domes
38	13	28.9	9	2	Q7X8P7_MAIZE	Q7X8P7 zea mays (m
39	13	28.9	9	2	Q56SS9_SAMCA	Q56SS9 sambucus ca
40	13	28.9	9	2	Q56ST0_9DIPS	Q56ST0 viburnum ut
41	13	28.9	9	2	Q56ST1_9DIPS	Q56ST1 viburnum ur
42	13	28.9	9	2	Q56ST2_9DIPS	Q56ST2 viburnum tr
43	13	28.9	9	2	Q56ST3_VIBOP	Q56ST3 viburnum op
44	13	28.9	9	2	Q56ST4_9DIPS	Q56ST4 viburnum ti
45	13	28.9	9	2	Q56ST5_9DIPS	Q56ST5 viburnum su

ALIGNMENTS

RESULT 1	Q7R8X5_PLAYO	Q7R8X5_PLAYO PRELIMINARY;	PRT;	9 AA.
AC	Q7R8X5;			
DT	01-MAR-2004 (Tremblrel. 26, Created)			
DT	01-MAR-2004 (Tremblrel. 26, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	Hypothetical protein.			
GN	Name=PY07095;			
OS	Plasmodium yoelii yoelii.			
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.			
OX	NCBI_TaxId=73239;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=17XNL;			
RX	MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;			
RA	Carlton J.M., Anguioni S.V., Suh B.B., Koij T.W., Petrea M.,			
RA	Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,			
RA	Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,			
RA	Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblum T.V.,			
RA	Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,			
RA	Florens L., Yates J.R., III, Raine J.D., Sinden R.E., Harris M.A.,			
RA	Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,			
RA	van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,			
RA	Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,			
RA	Carucci D.J.;			
RT	"Genome sequence and comparative analysis of the model rodent malaria			
RT	parasite Plasmodium yoelii yoelii.";			
RL	Nature 419:512-519 (2002).			
CC	-1- CAUTION: the sequence shown here is derived from an			
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is			
CC	preliminary data.			
DR	EMBL; ABL01002528; BAA19452.1; -; Genomic_DNA.			
KW	Hypothetical protein.			
SO	SEQUENCE 9 AA; 1013 MW; 4684D44724441E7 CR664;			
QY	Query Match	42.2%;	Score 19;	DB 2;
QY	Best Local Similarity	50.0%;	Pred. No. 2;	2e+06;
QY	Matches	3;	Conservative	3;
QY			Mismatches	0;
QY			Indels	0;
QY			Gaps	0;
QY	1 VLAHDL 6			
QY				
QY	1 MLHNNL 6			
DB				
DB	Q47556_ECOLI PRELIMINARY;		PRT;	9 AA.
DB	Q47556;			
DB	01-NOV-1996 (Tremblrel. 01, Created)			
DB	01-NOV-1996 (Tremblrel. 01, Last sequence update)			
DB	01-NOV-1998 (Tremblrel. 08, Last annotation update)			
DB	Aspartate transcarbamoylase regulatory chain (Fragment).			
DB	Name=PY11;			

OS Escherichia coli K12.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=83333;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=82275057; PubMed=7051000;
 RA Pauria C.D., Karels M.J., Navre M., Schachman H.K.;
 RT "Genes encoding Escherichia coli aspartate transcarbamoylase: the
 RT pyrB-pyri operon."
 RL Proc. Natl. Acad. Sci. U.S.A. 79:4020-4024(1982).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=83195078; PubMed=6302686;
 RA Hoover T.A., Roof W.D., Foltermann K.F., O'Donovan G.A., Bencini D.A.,
 RA Wild J.R.;
 RT "Nucleotide sequence of the structural gene (pyrB) that encodes the
 RT catalytic polypeptide of aspartate transcarbamoylase of Escherichia
 RT coli."
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2462-2466(1983).
 DR EMBL; J01670; AAA2475.1; -; Genomic_DNA.
 FT NON TER
 SQ SEQUENCE 9 AA; 1085 MW; 99BFD723344AA1F1 CRC64;

Query Match 42.2%; Score 19; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 HDDDL 8
 Db 3 HDNKLQ 8

RESULT 3
 ID Q28742_RABIT PRELIMINARY; PRT; 7 AA.
 AC Q28742;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DB Alpha-myosin heavy chain (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
 OC Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=84221901; PubMed=6328491;
 RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.J., Jokovic S.,
 RA Rabinowitz M.;
 RT "Characterization of genomic clones specifying rabbit alpha- and beta-
 RT ventricular myosin heavy chains."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
 DR EMBL; K01698; AAA31415.1; -; Genomic_DNA.
 DR PIR; I46868; I46868.
 FT NON TER
 SQ SEQUENCE 7 AA; 916 MW; 6B1B1A1E69326B0 CRC64;

Query Match 40.0%; Score 18; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 2.2e+06;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LHDD 5
 Db 3 WEDE 6

RESULT 4
 ID Q7M35_9TRYP PRELIMINARY; PRT; 9 AA.
 AC Q7M35;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Phosphoenolpyruvate carboxykinase.
 OS Trypanosoma brucei.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5691;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=95284106; PubMed=7766679; DOI=10.1016/0167-4838(95)00061-X;
 RA Hunt M., Koehler P.;
 RT "Purification and characterization of phosphoenolpyruvate
 RT carboxykinase from Trypanosoma brucei."
 RL Biochim. Biophys. Acta 1249:15-22(1995).
 DR PIR; S55696; S55696.
 SQ SEQUENCE 9 AA; 1063 MW; 35F2244331E05047 CRC64;

Query Match 37.8%; Score 17; DB 2; Length 9;
 Best Local Similarity 33.3%; Pred. No. 2.2e+06;
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLHDDL 6
 Db 3 IYKHL 8

RESULT 5
 ID O99182_9SMEG PRELIMINARY; PRT; 7 AA.
 AC O99182;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DB Cytochrome oxidase I (Fragment).
 GN Name=COI;
 OS Gnathobius zonatus.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Gnathobius.
 OX NCBI_TaxID=135316;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20072928; PubMed=10603257; DOI=10.1006/impv.1999.0656;
 RA Murphy W.J., Thomsen J.E., Collier G.E.;
 RT "Phylogeny of the Neotropical Killifish family Rivulidae
 RT (Cyprinodontiformes, Aplocheilidae) inferred from mitochondrial DNA
 RT sequences."
 RL Mol. Phylogenet. Evol. 13:289-301(1999).
 DR EMBL; AF002591; AAD01074.1; -; Genomic_DNA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER
 SQ SEQUENCE 7 AA; 899 MW; 672721F6CB572030 CRC64;

Query Match 35.6%; Score 16; DB 2; Length 7;
 Best Local Similarity 42.9%; Pred. No. 2.2e+06;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 VLHDDL 7
 Db 1 ILYOHL 7

RESULT 6
 ID Q7Z6G0_HUMAN PRELIMINARY; PRT; 8 AA.
 AC Q7Z6G0;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Fumarate hydratase (Fragment).
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Wei M.-H., Nickerson M.L., Toro J.R.,
 RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY299638; AAP57532.1; -; Genomic_DNA.
 FT NON TER 1
 FT NON TER 8
 SQ SEQUENCE 8 AA; 881 MW; 40CSBIE732C4330 CRC64;

Query Match 35.6%; Score 16; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLDL 3
 Db 4 VLDL 6

RESULT 7
 ID FAP8_MACRS STANDARD; PRT; 9 AA.
 AC P83281;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE FMRamide-like neuropeptide FLP8 (VSHNPLRF-amide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 OC Palaemonoidea; Palaemonidae; Macrobrachium.
 OX NCBI_TaxID=79674;
 RN [1]
 RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RX MEDLINE=21107394; PubMed=11179812; DOI=10.1016/S0196-9781(00)00382-X;
 RA Sathigorngul P., Sathithongkum W., Longyant S., Panchan N.,
 RA Sathigorngul W., Petsom A.,
 RT "Three more novel FMRamide-like neuropeptide sequences from the
 RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
 RL Peptides 22:191-197(2001).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MASS SPECTROMETRY: MW=1133.8; METHOD=MALDI; RANGE=1-9; NOTE=Ref.1.
 CC -1- SIMILARITY: Belongs to the FAP8 (FMRamide related peptide)
 CC family.

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 CC removed.

DR GO:0007218; P:neuropeptide signaling pathway; IDA.
 KW Annotation: Direct protein sequencing; Neuropeptide.
 FT MOD_RES 9
 FT MOD_RES 9 Phenylalanine amide.
 SQ SEQUENCE 9 AA; 1133 MW; 845A0729C44441F5 CRC64;

Query Match 35.6%; Score 16; DB 1; Length 9;
 Best Local Similarity 42.9%; Pred. No. 2.2e+06;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 VLDL 7
 Db 1 VSHNPL 7

RESULT 8
 ID Q70SM2_HUMAN
 AC Q70SM2_HUMAN PRELIMINARY; PRT; 9 AA.
 AC Q70SM2;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypermethylation in cancer 1 (Fragment).
 GN Name=Hic1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Mammary gland;
 RA Pine S., Guerardel C., Deltour S., Godwin A.K., Leprince D.,
 RT "Identification of a second G-C-rich promoter conserved in the human,
 RT murine and rat tumor suppressor genes Hic1."
 RL Oncogene 23:4023-4031(2004).
 DR EMBL; AJ550616; CAD79467.1; -; mRNA.
 FT NON TER 9
 FT NON TER 9
 SQ SEQUENCE 9 AA; 964 MW; 5B5E6DB1681AA7 CRC64;

Query Match 35.6%; Score 16; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 DLEA 9
 Db 3 DTMEA 7

RESULT 9
 ID Q4X981_PLACH PRELIMINARY; PRT; 9 AA.
 AC Q4X981;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PC404684.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5825;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlson J.M., Koof T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses."
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

DR EMBL; CNAJ01008648; CAH86543.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 9 AA; 1010 MW; 495F4441B6905727 CRC64;

Query Match 35.6%; Score 16; DB 2; Length 9;
 Best Local Similarity 16.7%; Pred. No. 2.2e+06;
 Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLDL 6
 Db 4 ITHNNV 9

RESULT 10
 ID Q8LPT5_MAIZE
 AC Q8LPT5_MAIZE PRELIMINARY; PRT; 9 AA.

AC Q8LPT5; 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Beta-expansin-like protein (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 NC NCBI_TaxID=4577;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
 RA Morgan M., Rafalski J.A.; EMBL/Genbank/DBJ databases.
 RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY094310; AAM21836.1; -; Genomic_DNA.
 FT NON TER 1
 SQ SEQUENCE 9 AA; 977 MW; 5C05BD2DCB1AAA3 CRC64;

Query Match 35.6%; Score 16; DB 2; Length 9;
 Best Local Similarity 33.3%; Pred. No. 2.2e+06;
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 4 DDLEA 9
 Db 4 DEVDA 9

RESULT 11
 P82568_STRPY PRELIMINARY; PRT; 9 AA.

AC P82568; 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE Unknown protein from 2D-page (Fragment).

OS Streptococcus pyogenes.
 OC Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.

RC STRAIN=US4;
 RA Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
 RA VanBogelen R.A.;
 RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
 RT proteins.";
 RL Submitted (MAY-2000) to Swiss-Prote.

CC -1- MASS SPECTROMETRY: MW=22592.04; METHOD=Electrospray.
 FT NON TER 1
 FT NON TER 9
 SQ SEQUENCE 9 AA; 1069 MW; 2A771042CB1AB2D7 CRC64;

Query Match 35.6%; Score 16; DB 2; Length 9;
 Best Local Similarity 40.0%; Pred. No. 2.2e+06;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 4 DDLE 8
 Db 4 DEVIE 8

RESULT 12

O15900_HUMAN PRELIMINARY; PRT; 8 AA.

AC O15900; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Homo sapiens (clone XP7B11A) (Fragment).

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Placenta;
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chnault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
 RA Caskey C.T.H.;
 RT "Isolation of chromosome-specific genes by reciprocal probing of
 RT arrayed cDNAs and cosmid libraries."
 RL Hum. Mol. Genet. 0:0-0(1995).
 DR EMBL; L32079; AAA73890.1; -; mRNA.
 FT NON TER 1
 FT NON TER 8
 SQ SEQUENCE 8 AA; 931 MW; B5DDC403369AAB1 CRC64;

Query Match 33.3%; Score 15; DB 2; Length 8;
 Best Local Similarity 42.9%; Pred. No. 2.2e+06;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 3 HDLEA 9
 Db 1 HCDMRA 7

RESULT 13
 O4XT27_PLACH PRELIMINARY; PRT; 8 AA.

AC O4XT27; 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=PC10664.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA Hall N., Karrae M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
 RA Bertram M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajadream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Jense C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).

CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAJ01003387; CAH79935.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 8 AA; 1050 MW; EFD801A04BSB11E6 CRC64;

Query Match 33.3%; Score 15; DB 2; Length 8;
 Best Local Similarity 28.6%; Pred. No. 2.2e+06;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 2 LHDDLE 8
 Db 1 MHEYTE 7

RESULT 14

O9XUN0_VYIRU PRELIMINARY; PRT; 9 AA.

AC O9XUN0; 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE P10 (Fragment).

OS Bacteriophage phi-10.

Search completed: April 6, 2006, 16:25:11
 Job time : 119 secs

OC Viruses; dsRNA viruses; Cystoviridae; Cystovirus.
 OX NCBI_TaxID=90889;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99350412; Pubmed=10419946;
 RA Mindich L., Qiao X., Qiao J., Onodera S., Romantschuk M.,
 RT Hoogstraaten D.;
 RT "Isolation of additional bacteriophages with genomes of segmented
 RT double-stranded RNA."
 RL J. Bacteriol. 181:4505-4508(1999).
 DR EMBL: AF125675; MAD2255.1; -; Genomic_RNA.
 FT NON_TER
 SQ SEQUENCE 9 AA; 1058 MW; 880E376AA720544A CRC64;

Query Match 33.3%; Score 15; DB 2; Length 9;
 Best Local Similarity 40.0%; Pred. No. 2.2e+06;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 4 DDLE 8
 |::|:
 Db 2 DNILD 6

RESULT 15
 TRPI_PSEPU
 ID TRPI_PSEPU STANDARD; PRT; 6 AA.
 AC P36414;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE HTH-type transcriptional regulator trpI (TrpBA operon transcriptional
 DE activator) (Fragment).
 GN Name=trpI;
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=303;
 RX [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=PR3 C18;
 RX MEDLINE=89335826; PubMed=2503057; DOI=10.1016/0300-9084(89)90183-1;
 RA Eberly L., Crawford I.P.;
 RT "DNA sequence of the tryptophan synthase genes of Pseudomonas
 RT putida."
 RL Biochimie 71:521-531(1989).
 CC -!- FUNCTION: Activates the expression of the trpBA genes encoding the
 CC two tryptophan synthase subunits. In the absence of the inducer
 CC (indoleglycerol phosphate), trpI binds upstream of the trpAB
 CC operon, overlapping its own promoter region.
 CC -!- SIMILARITY: Contains 1 HTH lyse-type DNA-binding domain.
 CC
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 CC
 CC EMBL: X13299; CAA31660.1; -; Genomic_DNA.
 DR InterPro; IPR000847; HTH_LYSE.
 DR PROSITE; PS50931; HTH_LYSE; PARTIAL.
 KW Activator; Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
 KW DNA-binding; Transcription; Transcription regulation;
 KW Tryptophan biosynthesis.
 FT NON_TER
 SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;

Query Match 31.1%; Score 14; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 HD 4
 | |
 Db 3 HD 4

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OM protein - protein search, using sw model

Run on: April 6, 2006, 16:25:31 ; Search time 27.333 Seconds
(without alignments)
27.222 Million cell updates/sec

Title: US-10-791-217A-2

Perfect score: 45
Sequence: 1 VLHDDLRA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 111694

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5 COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6 COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/ECTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	2	US-09-269-250E-20
2	45	100.0	9	2	US-09-489-760-2
3	37	82.2	9	2	US-09-269-250E-18
4	37	82.2	9	2	US-09-489-760-5
5	36	80.0	9	2	US-09-269-250E-29
6	36	80.0	9	2	US-09-489-760-1
7	30	66.7	9	2	US-09-489-760-4
8	28.5	63.3	8	2	US-09-269-250E-38
9	25	55.6	7	2	US-09-025-819-5
10	25	55.6	7	2	US-09-808-126-5
11	25	55.6	7	2	US-09-803-951-5
12	25	55.6	9	2	US-08-582-333A-3
13	25	55.6	9	2	US-09-305-923A-7
14	25	55.6	9	2	US-08-946-298-4
15	23	51.1	6	2	US-09-217-609A-8
16	23	51.1	6	2	US-08-873-235B-8
17	23	51.1	9	2	US-08-159-333A-370
18	22	48.9	5	2	US-08-811-463-30
19	22	48.9	5	2	US-09-933-497B-30
20	22	48.9	7	1	US-08-208-036-7
21	22	48.9	7	1	US-08-208-036-9
22	22	48.9	7	1	US-08-428-823-7
23	22	48.9	7	1	US-08-428-823-9
24	22	48.9	7	2	US-08-556-419-14
25	22	48.9	7	2	US-09-173-941-82
26	22	48.9	7	2	US-09-494-190-82
27	22	48.9	8	1	US-08-403-378B-13

28	22	48.9	9	2	US-09-217-609A-11	Sequence 11, Appl
29	22	48.9	9	2	US-08-873-235B-11	Sequence 11, Appl
30	21	46.7	6	1	US-08-459-568-20	Sequence 20, Appl
31	21	46.7	6	1	US-08-399-411-20	Sequence 20, Appl
32	21	46.7	6	2	US-08-516-859A-20	Sequence 20, Appl
33	21	46.7	6	2	US-09-586-472-20	Sequence 20, Appl
34	21	46.7	6	2	US-09-528-706-20	Sequence 20, Appl
35	21	46.7	8	1	US-08-459-568-75	Sequence 75, Appl
36	21	46.7	8	1	US-08-399-411-75	Sequence 75, Appl
37	21	46.7	8	2	US-08-516-859A-75	Sequence 75, Appl
38	21	46.7	8	2	US-09-419-826-1	Sequence 1, Appl
39	21	46.7	8	2	US-09-419-826-37	Sequence 37, Appl
40	21	46.7	8	2	US-09-586-472-75	Sequence 75, Appl
41	21	46.7	8	2	US-09-528-706-75	Sequence 75, Appl
42	21	46.7	9	1	US-07-671-757-30	Sequence 30, Appl
43	21	46.7	9	1	US-08-343-602-2	Sequence 2, Appl
44	21	46.7	9	1	US-08-459-568-72	Sequence 72, Appl
45	21	46.7	9	1	US-08-459-568-78	Sequence 78, Appl

ALIGNMENTS

```

RESULT 1
US-09-269-250E-20
; Sequence 20, Application US/09269250E
; Patent No. 6630883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elia
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-20

Query Match      100.0%; Score 45; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 VLHDDLRA 9
Db      1 VLHDDLRA 9

RESULT 2
US-09-489-760-2
; Sequence 2, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leiden
; APPLICANT: Goulmy, Elia A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-42850S
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL96/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Histocompatibility antigen

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US-09-489-760-2

Query Match 100.0%; Score 45; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
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 Db 1 VLHDDLLEA 9

RESULT 3

US-09-269-250E-18
 ; Sequence 18, Application US/09269250E
 ; Patent No. 6830883
 ; GENERAL INFORMATION:
 ; APPLICANT: Goulmy, Elsa
 ; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
 ; FILE REFERENCE: 58994
 ; CURRENT APPLICATION NUMBER: US/09/269,250E
 ; CURRENT FILING DATE: 1999-05-21
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 18
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
 US-09-269-250E-18

Query Match 82.2%; Score 37; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 4.6e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
 |||||
 Db 1 VLHDDLLEA 9

RESULT 4

US-09-489-760-5
 ; Sequence 5, Application US/09489760
 ; Patent No. 6878375
 ; GENERAL INFORMATION:
 ; APPLICANT: Rijksuniversiteit Te Leiden
 ; APPLICANT: Goulmy, Elsa A.J.M
 ; APPLICANT: Hunt, Donald F
 ; APPLICANT: Hard, Victor H
 ; TITLE OF INVENTION: The HA-1 Antigen
 ; FILE REFERENCE: 2183-4285US
 ; CURRENT APPLICATION NUMBER: US/09/489,760
 ; CURRENT FILING DATE: 2000-01-21
 ; EARLIER APPLICATION NUMBER: PCT/NL98/00424
 ; EARLIER FILING DATE: 1998-07-23
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: KIAA0223 partial complementary DNA
 US-09-489-760-5

Query Match 82.2%; Score 37; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 4.6e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
 |||||
 Db 1 VLHDDLLEA 9

RESULT 5

US-09-269-250E-29

; Sequence 29, Application US/09269250E
 ; Patent No. 6830883
 ; GENERAL INFORMATION:
 ; APPLICANT: Goulmy, Elsa
 ; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
 ; FILE REFERENCE: 58994
 ; CURRENT APPLICATION NUMBER: US/09/269,250E
 ; CURRENT FILING DATE: 1999-05-21
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 29
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (3)..(3)
 ; OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
 US-09-269-250E-29

Query Match 80.0%; Score 36; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 4.6e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
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 Db 1 VLHDDLLEA 9

RESULT 6

US-09-489-760-1
 ; Sequence 1, Application US/09489760
 ; Patent No. 6878375
 ; GENERAL INFORMATION:
 ; APPLICANT: Rijksuniversiteit Te Leiden
 ; APPLICANT: Goulmy, Elsa A.J.M
 ; APPLICANT: Hunt, Donald F
 ; APPLICANT: Hard, Victor H
 ; TITLE OF INVENTION: The HA-1 Antigen
 ; FILE REFERENCE: 2183-4285US
 ; CURRENT APPLICATION NUMBER: US/09/489,760
 ; CURRENT FILING DATE: 2000-01-21
 ; EARLIER APPLICATION NUMBER: PCT/NL98/00424
 ; EARLIER FILING DATE: 1998-07-23
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Histocompatibility antigen
 ; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (3)
 ; OTHER INFORMATION: AMINO ACID X REPRESENTS A HISTIDINE OR AN ARGININE
 ; OTHER INFORMATION: RESIDUE
 US-09-489-760-1

Query Match 80.0%; Score 36; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 4.6e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
 |||||
 Db 1 VLHDDLLEA 9

RESULT 7

US-09-489-760-4
 ; Sequence 4, Application US/09489760
 ; Patent No. 6878375
 ; GENERAL INFORMATION:
 ; APPLICANT: Rijksuniversiteit Te Leiden

APPLICANT: Goulmy, Elsa A.J.M
APPLICANT: Hunt, Donald F
APPLICANT: Hard, Victor H
TITLE OF INVENTION: The HA-1 Antigen
FILE REFERENCE: 2183-4285US
CURRENT APPLICATION NUMBER: US/09/489,760
CURRENT FILING DATE: 2000-01-21
EARLIER APPLICATION NUMBER: PCT/NL98/00424
EARLIER FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 9
TYPE: PRT
ORGANISM: Histocompatibility antigen
FEATURES:
NAME/KEY: PEPTIDE
LOCATION: (2)..(7)
OTHER INFORMATION: AMINO ACIDS X REPRESENT LEUCINE OR ISOLEUCINE
OTHER INFORMATION: RESIDUES
US-09-489-760-4

Query Match 66.7%; Score 30; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
| | | | |
DB 1 VHXDDXXEA 9

RESULT 8
US-09-269-250E-38
Sequence 38, Application US/09269250E
Patent No. 6830883
GENERAL INFORMATION:
APPLICANT: Goulmy, Elsa
TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
FILE REFERENCE: 58994
CURRENT APPLICATION NUMBER: US/09/269,250E
CURRENT FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 38
LENGTH: 8
TYPE: PRT
ORGANISM: HUMAN
US-09-269-250E-38

Query Match 63.3%; Score 28.5; DB 2; Length 8;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 VLHDDLLEA 9
| | | | |
DB 1 VLH-DLLEA 8

RESULT 9
US-09-025-819-5
Sequence 5, Application US/09025819
Patent No. 6225097
GENERAL INFORMATION:
APPLICANT: Odata, Shusei
APPLICANT: Nishino, Tokuzo
APPLICANT: Koyama, Tanetoshi
APPLICANT: Sato, Yoshihiro
TITLE OF INVENTION: DECAPRENTYL DIPHOSPHATE SYNTHETASE GENE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: KENYON & KENYON
STREET: 1500 K Street, N.W.
CITY: Washington

STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,819
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 251675
FILING DATE: 17-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Khalilian, Houri
REGISTRATION NUMBER: 39,546
REFERENCE/DOCKET NUMBER: 10235/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-220-4200
TELEFAX: 202-220-4201
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-025-819-5

Query Match 55.6%; Score 25; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHDD 5
| | | | |
DB 3 LHHDD 7

RESULT 10
US-09-808-126-5
Sequence 5, Application US/09808126
Patent No. 6410280
GENERAL INFORMATION:
APPLICANT: Odata, Shusei
APPLICANT: Nishino, Tokuzo
APPLICANT: Koyama, Tanetoshi
APPLICANT: Sato, Yoshihiro
TITLE OF INVENTION: DECAPRENTYL DIPHOSPHATE SYNTHETASE GENE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: KENYON & KENYON
STREET: 1500 K Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/808,126
FILING DATE: 08-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/025,819
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Khalilian, Houri
REGISTRATION NUMBER: 39,546

```

; REFERENCE/DOCKET NUMBER: 10235/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-220-4200
; TELEFAX: 202-220-4201
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-808-126-5

Query Match      55.6%; Score 25; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VLHDD 5
       :||||
       3 LHHDD 7

Db

RESULT 11
US-09-803-951-5
; Sequence 5, Application US/09803951
; Patent No. 6413761
; GENERAL INFORMATION:
; APPLICANT: Ohta, Shusei
; Nishino, Tokuzo
; Koyama, Tanetoshi
; Sato, Yoshihiro
; TITLE OF INVENTION: DECAPRENYL DIPHOSPHATE SYNTHETASE GENE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KENYON & KENYON
; STREET: 1500 K Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/803,951
; FILING DATE: 13-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/025,819
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Khalilian, Hourii
; REGISTRATION NUMBER: 39,546
; REFERENCE/DOCKET NUMBER: 10235/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-220-4200
; TELEFAX: 202-220-4201
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-803-951-5

Query Match      55.6%; Score 25; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 VLHDD 5
       :||||
       3 LHHDD 7

Db

RESULT 12
US-08-582-333A-3
; Sequence 3, Application US/08582333A
; Patent No. 6255059
; GENERAL INFORMATION:
; APPLICANT: Klein, Christine A.
; Applicant: Murphy, Andrew J. M.
; TITLE OF INVENTION: Methods and Compositions for
; IDENTIFYING RECEPTOR EFFECTORS
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Ascii(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/582,333A
; FILING DATE: 17-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine J. Kara
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: CPI-012CP5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
; US-08-582-333A-3

Query Match      55.6%; Score 25; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 4.6e+05;
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VLHDD 9
       :||||:|
       1 LHHDD 9

Db

RESULT 13
US-09-305-923A-7
; Sequence 7, Application US/09305923A
; Patent No. 6355473
; GENERAL INFORMATION:
; APPLICANT: Oostanin, Kiriill
; Applicant: Silverman, Lauren
; TITLE OF INVENTION: YEAST CELLS HAVING MUTATIONS IN etp22 AND USES THEREFOR
; FILE REFERENCE: CPI-091
; CURRENT APPLICATION NUMBER: US/09/305,923A
; CURRENT FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: 60/084,420
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
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LENGTH: 9
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-305-923A-7

Query Match 55.6%; Score 25; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 4.6e+05;
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 VHADDLER 9
DB 1 LIHEDIAXA 9

RESULT 14
US-08-946-298-4
Sequence 4, Application US/08946298A
Patent No. 6864060
GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: YEAST CELLS EXPRESSING MODIFIED G PROTEINS AND METHODS
FILE REFERENCE: CPT-012CP8
CURRENT APPLICATION NUMBER: US/08/946,298A
EARLIER FILING DATE: 1997-10-07
EARLIER APPLICATION NUMBER: 08/689,172
EARLIER FILING DATE: 1996-08-06
EARLIER APPLICATION NUMBER: 08/582,333
EARLIER FILING DATE: 1996-01-17
EARLIER APPLICATION NUMBER: 08/463,181
EARLIER FILING DATE: 1995-06-05
EARLIER APPLICATION NUMBER: 08/322,137
EARLIER FILING DATE: 1994-10-13
EARLIER APPLICATION NUMBER: 08/309,313
EARLIER FILING DATE: 1994-09-20
EARLIER APPLICATION NUMBER: 08/190,328
EARLIER FILING DATE: 1994-01-31
EARLIER APPLICATION NUMBER: 08/041,431
EARLIER FILING DATE: 1993-03-31
NUMBER OF SEQ ID NOS: 86
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 9
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-08-946-298-4

Query Match 55.6%; Score 25; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 4.6e+05;
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 VHADDLER 9
DB 1 LIHEDIAXA 9

RESULT 15
US-09-217-609A-8
Sequence 8, Application US/09217609A
Patent No. 6071733
GENERAL INFORMATION:
APPLICANT: MURAMATSU, Masayoshi
APPLICANT: KOIKE, Ayumi
APPLICANT: OGURA, Kyoza
APPLICANT: KOYAMA, Tanetoshi
APPLICANT: SHIMIZU, Naoto
APPLICANT: CHO, Yewwin
TITLE OF INVENTION: Prenyl Diphosphate Synthetase Genes
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, NW - Suite 600
CITY: Washington

STATE: DC
COUNTRY: US
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: Wordperfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,609A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/873,235
FILING DATE: 11-Jun-1997
ATTORNEY/AGENT INFORMATION:
NAME: TOPFENETTY, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 10235/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-217-609A-8

Query Match 51.1%; Score 23; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHADDD 5
DB 2 LIHDD 6

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GenCore version 5.1.7
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Title: US-10-791-217A-2

Perfect score: 45

Sequence: 1 VLHDDLRA 9

Scoring table: BLOSUM62
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Searched: 1867569 seqs, 417829326 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	4 US-10-623-176-2	Sequence 2, Appl
2	45	100.0	9	4 US-10-791-217-2	Sequence 2, Appl
3	45	100.0	9	5 US-10-861-335-1	Sequence 1, Appl
4	45	100.0	9	4 US-11-007-740-20	Sequence 20, Appl
5	41	91.1	9	4 US-10-623-176-41	Sequence 40, Appl
6	41	91.1	9	4 US-10-623-176-45	Sequence 45, Appl
7	37	82.2	9	4 US-10-623-176-10	Sequence 10, Appl
8	37	82.2	9	4 US-10-623-176-47	Sequence 47, Appl
9	37	82.2	9	4 US-10-791-217-5	Sequence 5, Appl
10	37	82.2	9	6 US-11-007-740-18	Sequence 18, Appl
11	36	80.0	9	4 US-10-623-176-1	Sequence 1, Appl
12	36	80.0	9	4 US-10-623-176-40	Sequence 40, Appl
13	36	80.0	9	4 US-10-791-217-1	Sequence 1, Appl
14	36	80.0	9	6 US-11-007-740-29	Sequence 29, Appl
15	33	73.3	9	4 US-10-623-176-42	Sequence 42, Appl
16	33	73.3	9	4 US-10-623-176-46	Sequence 46, Appl
17	32	71.1	9	4 US-10-623-176-4	Sequence 4, Appl
18	30	66.7	9	4 US-10-623-176-14	Sequence 14, Appl
19	30	66.7	9	4 US-11-007-740-4	Sequence 4, Appl
20	30	66.7	9	6 US-11-007-740-40	Sequence 40, Appl
21	29	64.4	9	4 US-10-623-176-48	Sequence 48, Appl
22	28.5	63.3	8	4 US-10-623-176-15	Sequence 15, Appl
23	28.5	63.3	8	6 US-11-007-740-38	Sequence 38, Appl
24	28	62.2	9	4 US-10-623-176-23	Sequence 23, Appl
25	28	62.2	9	4 US-10-623-176-38	Sequence 38, Appl
26	28	62.2	9	4 US-10-777-053-95	Sequence 95, Appl
27	28	62.2	9	4 US-10-837-217-95	Sequence 95, Appl

28	27	60.0	9	5 US-10-705-459-280	Sequence 280, App
29	26	57.8	6	4 US-10-166-225A-163	Sequence 163, App
30	26	57.8	6	4 US-10-166-225A-164	Sequence 164, App
31	26	57.8	6	4 US-10-166-225A-165	Sequence 165, App
32	26	57.8	6	4 US-10-166-225A-166	Sequence 166, App
33	26	57.8	6	4 US-10-825-026-48	Sequence 48, Appl
34	25	55.6	6	4 US-10-166-225A-161	Sequence 161, App
35	25	55.6	6	4 US-10-166-225A-162	Sequence 162, App
36	25	55.6	7	3 US-09-803-951-5	Sequence 5, Appl
37	25	55.6	9	3 US-09-747-774A-3	Sequence 3, Appl
38	25	55.6	9	3 US-09-953-354-3	Sequence 3, Appl
39	25	55.6	9	4 US-10-267-074-14	Sequence 14, Appl
40	25	55.6	9	4 US-10-267-074-16	Sequence 16, Appl
41	25	55.6	9	5 US-10-752-478-3	Sequence 3, Appl
42	25	55.6	9	5 US-10-967-087-4	Sequence 4, Appl
43	24	53.3	7	4 US-10-020-354-86	Sequence 86, Appl
44	24	53.3	8	5 US-10-808-187-462	Sequence 462, App
45	24	53.3	8	5 US-10-807-807-462	Sequence 462, App

ALIGNMENTS

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RESULT 1
US-10-623-176-2
; Sequence 2, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elie A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: 11..(9)
US-10-623-176-2

Query Match          100.0%; Score 45; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CQ      1 VLHDDLRA 9
DB      1 VLHDDLRA 9

RESULT 2
US-10-791-217-2
; Sequence 2, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elie A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H
```

```

; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/10/791,217
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: obtained from histocompatibility antigen
US-10-791-217-2
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```

Query Match          100.0%; Score 45; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 VLHDDLLEA 9
        |||||
Db       1 VLHDDLLEA 9
```

```

RESULT 3
US-10-861-335-1
; Sequence 1, Application US/10661335
; Publication No. US20050031612A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa A.J.M.
; TITLE OF INVENTION: Minor histocompatibility antigen HA-1: target antigen for immunot
; FILE REFERENCE: 2183-6479US
; CURRENT APPLICATION NUMBER: US/10/861,335
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: PCT/NL02/00791
; PRIOR FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: EP 01204704.9
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HA-1 peptide
US-10-861-335-1
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```

Query Match          100.0%; Score 45; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 VLHDDLLEA 9
        |||||
Db       1 VLHDDLLEA 9
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```

RESULT 4
US-11-007-740-20
; Sequence 20, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 2799/58994-A
; CURRENT APPLICATION NUMBER: US/11/007,740
; CURRENT FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: 09/269,250
; PRIOR FILING DATE: 1999-05-21
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; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-20
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```

Query Match          100.0%; Score 45; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 VLHDDLLEA 9
        |||||
Db       1 VLHDDLLEA 9
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RESULT 5
US-10-623-176-41
; Sequence 41, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-41
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```

Query Match          91.1%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VLHDDLLE 8
        |||||
Db       2 VLHDDLLE 9
```

```

RESULT 6
US-10-623-176-45
; Sequence 45, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
```

PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 45
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(9)
US-10-623-176-45

Query Match 91.1%; Score 37; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LHDDLLEA 9
Db 1 LHDDLLEA 8

RESULT 7
US-10-623-176-10
Sequence 10, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Els A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 10
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(9)
US-10-623-176-10

Query Match 82.2%; Score 37; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VHDDLLEA 9
Db 1 VHDDLLEA 9

RESULT 8

US-10-623-176-47
Sequence 47, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Els A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 47
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(9)
US-10-623-176-47

Query Match 82.2%; Score 37; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 HDDLLEA 9
Db 1 HDDLLEA 7

RESULT 9
US-10-791-217-5
Sequence 5, Application US/10791217
Publication No. US20040191268A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Elsa A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: The HA-1 Antigen
FILE REFERENCE: 2183-4285US
CURRENT APPLICATION NUMBER: US/10/791,217
CURRENT FILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: US/09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 5
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: obtained from KIAA0223 partial complementary DNA
US-10-791-217-5

Query Match 82.2%; Score 37; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VHDDLLEA 9

Db 1 VLXDDLEA 9

```
RESULT 10
US-11-007-740-18
; Sequence 18, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 2799/58994-A
; CURRENT APPLICATION NUMBER: US/11/007,740
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: 09/269,250
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-18
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```
Query Match      82.2%; Score 37; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 1 VLXDDLEA 9
Db 1 VLXDDLEA 9

```
RESULT 11
US-10-623-176-1
; Sequence 1, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; OTHER INFORMATION: wherein X can be R or H
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-1
```

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Query Match      80.0%; Score 36; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 1 VLXDDLEA 9

Db 1 VLXDDLEA 9

```
RESULT 12
US-10-623-176-40
; Sequence 40, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-40
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Query Match      80.0%; Score 36; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 VLXDDLEA 7
Db 3 VLXDDLEA 9

```
RESULT 13
US-10-791-217-1
; Sequence 1, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/10/791,217
; PRIOR FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: obtained from histocompatibility antigen
; NAME/KEY: MISC FEATURE
; LOCATION: (3)..(3)
```


OTHER INFORMATION: Xaa is HISTIDINE OR ARGININE RESIDUE
US-10-791-217-1

Query Match 80.0%; Score 36; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
|||
Db 1 VLXDDLLEA 9

RESULT 14

US-11-007-740-29
Sequence 29, Application US/11007740
Publication No. US20050233350A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Elise
TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
FILE REFERENCE: 2799/58994-A
CURRENT APPLICATION NUMBER: US/11/007,740
CURRENT FILING DATE: 2004-12-08
PRIOR APPLICATION NUMBER: 09/269,250
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 9
TYPE: PRT
ORGANISM: Human
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (3)-(3)
OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
US-11-007-740-29

Query Match 80.0%; Score 36; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
|||
Db 1 VLXDDLLEA 9

RESULT 15

US-10-623-176-42
Sequence 42, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Elise A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 42
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide

FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(9)
US-10-623-176-42

Query Match 73.3%; Score 33; DB 4; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLLE 8
|||
Db 2 VLXDDLLE 9

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Title: US-10-791-217A-2

Perfect score: 45

Sequence: 1 VLHDDLRA 9

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Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0*

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8: /SIDSS/ptodata/2/pubppa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	7	US-11-010-748A-11 Sequence 11, Appl
2	37	82.2	9	7	US-11-010-748A-12 Sequence 12, Appl
3	26	57.8	6	7	US-11-129-143-163 Sequence 163, Appl
4	26	57.8	6	7	US-11-129-143-164 Sequence 164, Appl
5	26	57.8	6	7	US-11-129-143-165 Sequence 165, Appl
6	25	55.6	6	7	US-11-129-143-166 Sequence 166, Appl
7	25	55.6	6	7	US-11-129-143-161 Sequence 161, Appl
8	25	55.6	6	7	US-11-129-143-162 Sequence 162, Appl
9	24	53.3	6	7	US-11-004-399-1155 Sequence 1155, Appl
10	23	51.1	6	6	US-10-485-788A-353 Sequence 353, Appl
11	23	51.1	6	6	US-10-485-788A-354 Sequence 354, Appl
12	23	51.1	8	6	US-10-485-788A-355 Sequence 355, Appl
13	23	51.1	9	7	US-11-033-039-785 Sequence 785, Appl
14	23	51.1	9	7	US-11-033-039-809 Sequence 809, Appl
15	22	48.9	5	6	US-10-485-788A-332 Sequence 332, Appl
16	22	48.9	6	6	US-10-857-435A-443 Sequence 443, Appl
17	22	48.9	7	6	US-10-982-440-126 Sequence 126, Appl
18	22	48.9	8	7	US-11-045-024-444 Sequence 444, Appl
19	22	48.9	8	7	US-11-045-024-5467 Sequence 5467, Appl
20	22	48.9	8	7	US-11-045-024-7094 Sequence 7094, Appl
21	22	48.9	9	7	US-11-045-024-607 Sequence 607, Appl
22	22	48.9	9	7	US-11-045-024-3715 Sequence 3715, Appl
23	22	48.9	9	7	US-11-045-024-5511 Sequence 5511, Appl
24	22	48.9	9	7	US-11-045-024-12585 Sequence 12585, Appl
25	22	48.9	9	7	US-11-045-024-14029 Sequence 14029, Appl

26	21	46.7	4	6	US-10-485-788A-351 Sequence 351, Appl
27	21	46.7	7	6	US-10-510-155-28 Sequence 28, Appl
28	20	44.4	4	6	US-10-667-295-263 Sequence 263, Appl
29	20	44.4	4	6	US-10-857-435A-366 Sequence 366, Appl
30	20	44.4	4	7	US-11-019-027-5 Sequence 5, Appl
31	20	44.4	4	7	US-11-174-413-64 Sequence 64, Appl
32	20	44.4	4	7	US-11-108-088-69 Sequence 69, Appl
33	20	44.4	4	7	US-11-033-030-3 Sequence 3, Appl
34	20	44.4	5	7	US-11-129-143-168 Sequence 168, Appl
35	20	44.4	5	7	US-11-129-143-169 Sequence 169, Appl
36	20	44.4	5	7	US-11-129-143-170 Sequence 170, Appl
37	20	44.4	5	7	US-11-129-143-171 Sequence 171, Appl
38	20	44.4	5	7	US-11-129-143-172 Sequence 172, Appl
39	20	44.4	5	7	US-11-129-143-173 Sequence 173, Appl
40	20	44.4	6	6	US-10-857-435A-367 Sequence 367, Appl
41	20	44.4	6	6	US-10-857-435A-397 Sequence 397, Appl
42	20	44.4	6	6	US-10-857-435A-667 Sequence 667, Appl
43	20	44.4	8	7	US-11-021-305-62 Sequence 62, Appl
44	20	44.4	8	7	US-11-021-305-65 Sequence 65, Appl
45	20	44.4	8	7	US-11-021-305-66 Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-11-010-748A-11
Sequence 11, Application US/11010748A
Publication No. US20050244421A1
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMAYER, Wolfgang
APPLICANT: MOLL, Heidrun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
FILE REFERENCE: MER-136
CURRENT APPLICATION NUMBER: US/11/010,748A
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/EP03/06251
PRIOR FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: EP02013423.5
PRIOR FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 926
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(9)
OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
US-11-010-748A-11
Query Match 100.0%; Score 45; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLHDDLRA 9
DB 1 VLHDDLRA 9
RESULT 2
US-11-010-748A-12
Sequence 12, Application US/11010748A
Publication No. US20050244421A1
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMAYER, Wolfgang
APPLICANT: MOLL, Heidrun
APPLICANT: SCHARM, Burkhard

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T
; OTHER INFORMATION: ell epitopes
US-11-010-748A-12
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Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db      1 VLDDLLEA 9
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RESULT 3
US-11-129-143-163
; Sequence 163, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Bacillus stearoothermophilus
US-11-129-143-163
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Query Match      57.8%; Score 26; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      2 IHDDL 6
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Db      1 IHDDL 5
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RESULT 4
US-11-129-143-164
; Sequence 164, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
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; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 164
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-11-129-143-164
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Query Match      57.8%; Score 26; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      2 IHDDL 6
        :|||||
Db      1 IHDDL 5
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RESULT 5
US-11-129-143-165
; Sequence 165, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 165
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-129-143-165
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Query Match      57.8%; Score 26; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      2 IHDDL 6
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Db      1 IHDDL 5
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RESULT 6
US-11-129-143-166
; Sequence 166, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
; LENGTH: 6
; TYPE: PRT
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/ ORGANISM: Haemophilus influenzae
US-11-129-143-166

Query Match 57.8%; Score 26; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHDDL 6
:||||
Db 1 IHDDL 5

RESULT 7

US-11-129-143-161
/ Sequence 161, Application US/11129143
/ Publication No. US20050266516A1
/ GENERAL INFORMATION:
/ APPLICANT: BERRY, Alan
/ APPLICANT: BRETZEL, Werner
/ APPLICANT: HUMBELIN, Markus
/ APPLICANT: LOPEZ-ULIBARRI, Rual
/ APPLICANT: MAYER, Anne F.
/ APPLICANT: YELISEV, Alexei A.
/ TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
/ FILE REFERENCE: C38435/121966
/ CURRENT APPLICATION NUMBER: US/11/129,143
/ CURRENT FILING DATE: 2005-05-13
/ NUMBER OF SEQ ID NOS: 197
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 161
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Bradyrhizobium japonicum
US-11-129-143-161

Query Match 55.6%; Score 25; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHDDL 6
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Db 1 VHDDL 5

RESULT 8

US-11-129-143-162
/ Sequence 162, Application US/11129143
/ Publication No. US20050266516A1
/ GENERAL INFORMATION:
/ APPLICANT: BERRY, Alan
/ APPLICANT: BRETZEL, Werner
/ APPLICANT: HUMBELIN, Markus
/ APPLICANT: LOPEZ-ULIBARRI, Rual
/ APPLICANT: MAYER, Anne F.
/ APPLICANT: YELISEV, Alexei A.
/ TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
/ FILE REFERENCE: C38435/121966
/ CURRENT APPLICATION NUMBER: US/11/129,143
/ CURRENT FILING DATE: 2005-05-13
/ NUMBER OF SEQ ID NOS: 197
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 162
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Rhizobium sp. strain NGR234
US-11-129-143-162

Query Match 55.6%; Score 25; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHDDL 6
:||||

Db 1 VHDDL 5

RESULT 9
US-11-004-399-1155
/ Sequence 1155, Application US/11004399
/ Publication No. US20060053516A1
/ GENERAL INFORMATION:
/ APPLICANT: Chye, Mee Lee
/ APPLICANT: Li, Hong Ye
/ APPLICANT: Ramalingam, Sathiskumar
/ APPLICANT: Poon, Leo Lit Man
/ APPLICANT: Peiris, Joseph Sriyal Malik
/ TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-Cov Viral Nucleotide
/ FILE REFERENCE: Sequences and Methods of Use Thereof for Immunization Against S
/ FILE REFERENCE: 2587/73166/RDK
/ CURRENT APPLICATION NUMBER: US/11/004,399
/ CURRENT FILING DATE: 2004-12-03
/ PRIOR APPLICATION NUMBER: US 60/527,637
/ PRIOR FILING DATE: 2003-12-03
/ NUMBER OF SEQ ID NOS: 4043
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 1155
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: SARS-Cov Virus
US-11-004-399-1155

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Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHDD 5
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Db 3 LHDD 6

RESULT 10
US-10-485-788A-353
/ Sequence 353, Application US/10485788A
/ Publication No. US20050282743A1
/ GENERAL INFORMATION:
/ APPLICANT: Lu, Peter S.
/ APPLICANT: Rabinowitz, Joshua D.
/ APPLICANT: Schweizer, Johannes
/ APPLICANT: Carrick, Deanna Marie
/ APPLICANT: Arbor Vita Corporation
/ TITLE OF INVENTION: Molecular Interactions in Cells
/ FILE REFERENCE: 20054-003320US
/ CURRENT APPLICATION NUMBER: US/10/485,788A
/ CURRENT FILING DATE: 2004-02-03
/ PRIOR APPLICATION NUMBER: US 60/309,841
/ PRIOR FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: US 60/360,061
/ PRIOR FILING DATE: 2002-02-25
/ PRIOR APPLICATION NUMBER: WO PCT/US02/24655
/ PRIOR FILING DATE: 2002-08-02
/ NUMBER OF SEQ ID NOS: 841
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 353
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-485-788A-353

Query Match 51.1%; Score 23; DB 6; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHDDL 6
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Db 1 LVHDDV 6

RESULT 11
US-10-485-788A-354
; Sequence 354, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; PRIOR FILING DATE: 2004-02-03/309,841
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 354
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-354

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Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVHDDL 6
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Db 2 LVHDDV 7

RESULT 12
US-10-485-788A-355
; Sequence 355, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; PRIOR FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 355
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-355

Query Match 51.1%; Score 23; DB 6; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVHDDL 6
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Db 3 LVHDDV 8

RESULT 13
US-11-033-039-785
; Sequence 785, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 785
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Zaire ebolavirus
US-11-033-039-785

Query Match 51.1%; Score 23; DB 7; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.4e+05;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LVHDDLLEA 9
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Db 1 LVHSTLKA 9

RESULT 14
US-11-033-039-809
; Sequence 809, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 809
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Zaire ebolavirus
US-11-033-039-809

Query Match 51.1%; Score 23; DB 7; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.4e+05;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LVHDDLLEA 9
:|:|:|:|:
Db 1 LVHSTLKA 9

RESULT 15
US-10-485-788A-352
; Sequence 352, Application US/10485788A

; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Atbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 352
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-352

Query Match 48.9%; Score 22; DB 6; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 1 VHDDV 5

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:12:46 ; Search time 111.667 Seconds
(without alignments)
35.413 Million cell updates/sec

Title: US-10-791-217A-5

Perfect score: 42

Sequence: 1 VLRDDLEA 9

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Gapop 10.0 , Gapext 0.5

Searched: 244163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 401289

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 10%

Listing first 45 summaries

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7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	42	100.0	9	2	AAW99197	Aaw99197 Minor his
2	42	100.0	9	2	AAW97374	Aaw97374 HA-1 R-al
3	42	100.0	9	8	ADH40334	Adh40334 Human min
4	37	88.1	9	2	AAW99196	Aaw99196 Minor his
5	37	88.1	9	2	AAW97375	Aaw97375 HA-1 H-al
6	37	88.1	9	8	ADH40333	Adh40333 Human min
7	36	85.7	9	2	AAW99195	Aaw99195 Minor his
8	36	85.7	9	2	AAW97572	Aaw97572 T-cell ep
9	29	69.0	9	8	ADT73023	Adt73023 Human RSV
10	27	64.3	9	2	AAW47427	Aaw47427 Prey1 d1
11	26	61.9	9	8	ADT73690	Adt73690 Human RSV
12	26	61.9	9	8	ADT72767	Adt72767 Human RSV
13	25	59.5	9	5	AAU71428	Aau71428 Human MHC
14	25	59.5	9	8	ADT72766	Adt72766 Human RSV
15	25	59.5	9	8	ADT73689	Adt73689 Human RSV
16	24	57.1	9	7	AAAB1550	Aaab1550 Zif268 z1
17	24	57.1	9	7	ADMI8256	Admi8256 C trachom
18	24	57.1	9	5	ADMI8218	Admi8218 Chlamydia
19	23	54.8	9	5	AAU71211	Aau71211 Human MHC
20	23	54.8	9	6	ABR19961	Abri19961 Human can
21	23	54.8	9	6	ABR19426	Abri19426 Human can
22	23	54.8	9	6	ABR18988	Abri18988 Human can
23	23	54.8	9	6	ABR19578	Abri19578 Human can
24	23	54.8	9	6	ABR19174	Abri19174 Human can

25	23	54.8	9	6	ABR19780	Abri19780 Human can
26	23	54.8	9	8	ADU99853	Adu99853 BC24 tumo
27	23	54.8	9	8	ABY01546	Abiy01546 SARS coro
28	23	54.8	9	9	ADZ50925	Adz50925 Y. pestis
29	22	52.4	9	2	AAW97373	Aaw97373 Peptide e
30	22	52.4	9	8	ADP72091	Adp72091 Rabbit pe
31	22	52.4	9	8	ABY01413	Abiy01413 SARS coro
32	22	52.4	9	9	ADM23047	Adm23047 SARS coro
33	21	50.0	4	9	ABE31418	Aeb31418 Endoplasm
34	21	50.0	6	3	AAI12035	Aai12035 Peptide #
35	21	50.0	6	5	AAU08010	Aau08010 Rat Rb-in
36	21	50.0	6	7	ADP84629	Adp84629 Mammalia
37	21	50.0	7	5	ABP48411	Abp48411 Zinc fing
38	21	50.0	7	5	ABP48419	Abp48419 Zinc fing
39	21	50.0	7	5	ABP48419	Abp48419 Zinc fing
40	21	50.0	7	5	ABG79371	Abg79371 Zinc fing
41	21	50.0	7	6	ABP96179	Abp96179 Zinc fing
42	21	50.0	7	7	ADA62240	Ada62240 Zinc fing
43	21	50.0	7	7	ADA62237	Ada62237 Zinc fing
44	21	50.0	7	7	ADA62245	Ada62245 Zinc fing
45	21	50.0	7	7	ADM20449	Adm20449 Synthetic

ALIGNMENTS

RESULT 1
AAW99197
ID AAW99197 standard; peptide; 9 AA.
XX
AC AAW99197;
XX
DT 20-MAY-1999 (first entry)
XX
DE Minor histocompatibility antigen HA-1 T-cell epitope #3.
XX
DE Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
XX
KM Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
XX
KM graft versus host disease; bone marrow transplant; leukaemia; vaccine;
XX
KM diagnosis; aplastic anaemia; immune deficiency disease.
XX
XX Homo sapiens.
XX
OS Homo sapiens.
XX
XX MO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WC-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
XX (UYLE-) RIKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
XX WPI; 1999-153312/13.
XX
DR A new minor histocompatibility antigen, HA-1 - useful to treat immune
XX
XX diseases and prevent rejection and host versus graft disease in bone
XX
XX marrow and organ transplantation.
XX
XX Disclosure; Page 15; 47pp; English.
XX
XX The present sequence represents a new peptide (p1) constituting a T-cell
XX
XX epitope obtainable from the minor histocompatibility antigen HA-1. The
XX
XX peptide is immunogenic and can be used as part of a vaccine. p1 is used
XX
XX as a medicine, to induce tolerance for transplants, prevent rejection
XX
XX and/or graft versus host disease, or to treat (auto) immune diseases. In
XX
XX particular it can be used with bone marrow transplantation, in the
XX
XX treatment of severe aplastic anaemia, leukaemia, and immune deficiency
XX
XX diseases
XX
XX Sequence 9 AA;

Query Match 100.0%; Score 42; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

RESULT 2
 AAW97374

ID AAW97374 standard; protein; 9 AA.

AC AAW97374;

DT 13-MAY-1999 (first entry)

DE HA-1 R-allele sequence.

XX Intron; minor histocompatibility antigen HA-1; typing allele; H allele;

KM R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;

KW severe aplastic anaemia; leukaemia; immune deficiency disease; ss.

XX Homo sapiens.

XX MO9905313-A2.

XX 04-FEB-1999.

XX 23-JUL-1998; 98WO-EP004928.

XX 23-JUL-1997; 97EP-00202303.

XX 02-JUN-1998; 98EP-00870125.

XX (UYLE-) RICKSUNIV LEIDEN.

XX Goulmy E;

XX WPI; 1999-142960/12.

XX Typing minor histocompatibility antigen HA-1 - by amplifying and

XX identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection

XX of genetic aberrances.

XX Claim 13; Fig 5; 59pp; English.

XX The present sequence represents part of the minor histocompatibility

XX antigen HA-1 R-allele. The specification describes methods for typing

XX alleles (preferably the H and R alleles) of the minor histocompatibility

XX antigen HA-1 in a sample, which comprise detecting polymorphic

XX nucleotides in the cDNA or genomic nucleic acids of the alleles. The

XX methods can be used for HA-1 typing for bone marrow transplants, severe

XX aplastic anaemia, leukaemia and immune deficiency diseases, as well as

XX detection of genetic aberrances. The probes and primers of the invention

XX can be used to screen for the HA-1 alleles. The HA-1 peptides can be used

XX anti-idiotypic B cells and/or T cells and antibodies

XX Sequence 9 AA;

XX Query Match 100.0%; Score 42; DB 2; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 11-MAR-2004 (first entry)

XX Human minor histocompatibility antigen HA-1 T cell epitope.

XX human; cytotoxic; vaccine; SNP profile; cancer; leukaemia;

XX minor histocompatibility antigen; mRNA; T cell epitope.

XX Homo sapiens.

XX WO2003106692-A2.

XX 24-DEC-2003.

XX 13-JUN-2003; 2003WO-EP006251.

XX 13-JUN-2002; 2002EP-00013423.

XX (MERE) MERCK PATENT GMBH.

XX Strittmatter W, Moll H;

XX WPI; 2004-082200/08.

XX Providing allelic variant epitope of protein based on single nucleotide

XX polymorphism by defining target protein, screening database of protein,

XX identifying, selecting allelic variant protein, creating variant

XX epitopes.

XX Disclosure; Page 82; 119pp; English.

XX The invention relates to a novel method for providing epitopes of allelic

XX variants of antigenic proteins from specific species based on single

XX nucleotide polymorphism (SNP), by defining target protein/peptide or its

XX subset, screening database of DNA encoding target protein, identifying,

XX selecting allelic peptide/protein variants, expression product or its

XX fragment encoded by DNA sequence having SNP, creating variant epitopes,

XX selecting epitopes binding to MHC protein. A protein of the invention has

XX cytosolic activity, and may have a use in a vaccine. The method is

XX useful for generating a SNP profile of one or more individuals from a

XX given species by applying the method for several protein from the

XX individuals, where the SNP profile was related to disease, preferably

XX cancer. This is useful for diagnosing a disease in an individual by

XX generating the SNP-related polymorphic profile. A method of the invention

XX is useful for transplanting haematopoietic stem cells from a donor to a

XX recipient and treating cancer, preferably leukaemia, and for determining

XX the progression, regression or onset of a treated disease. The present

XX sequence is used in the exemplification of the invention.

XX Sequence 9 AA;

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VLKDDLLA 9
 |||||
 DB 1 VLKDDLLA 9

XX Query Match 100.0%; Score 42; DB 8; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX OS Homo sapiens.
 XX X MO9905174-A1.
 XX PN
 XX PD 04-FEB-1999.
 XX PF 23-JUL-1998; 98WO-NL000425.
 XX PR 23-JUL-1997; 97EP-00202303.
 XX PA (UYLB-) RIKKSUNIV LEIDEN.
 XX PI Goulmy EAJM, Hunt DF, Engelhard VH;
 XX DR WPI; 1999-153312/13.
 XX PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
 PT diseases and prevent rejection and host versus graft disease in bone
 PT marrow and organ transplantation.
 XX PS Claim 3; Page 32; 47pp; English.
 XX CC The present sequence represents a new peptide (P1) constituting a T-cell
 CC epitope obtainable from the minor histocompatibility antigen HA-1. The
 CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
 CC as a medicine, to induce tolerance for transplants, prevent rejection
 CC and/or graft versus host disease, or to treat (auto) immune diseases. In
 CC particular it can be used with bone marrow transplantation, in the
 CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
 CC diseases
 XX SQ Sequence 9 AA;

Query Match 88.1%; Score 37; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VRDDLLRA 9
 |||||
 Db 1 VLHDDLLRA 9

RESULT 5
 ID AAM97375 standard; protein; 9 AA.
 AC AAM97375;
 XX
 DT 13-MAY-1999 (first entry)
 XX
 DE HA-1 H-allele sequence.
 XX
 KM Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
 KM R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
 KM severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9905313-A2.
 XX
 PD 04-FEB-1999.
 XX
 PF 23-JUL-1998; 98WO-EP004928.
 XX
 PR 23-JUL-1997; 97EP-00202303.
 PR 02-JUN-1998; 98EP-00870125.
 XX
 PA (UYLB-) RIKKSUNIV LEIDEN.
 XX
 PI Goulmy B;
 XX
 DR WPI; 1999-142960/12.

XX PT Typing minor histocompatibility antigen HA-1 - by amplifying and
 PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
 PT of genetic aberrances.
 XX
 XX
 XX Claim 10; Fig 5; 59pp; English.

XX CC The present sequence represents part of the minor histocompatibility
 CC antigen HA-1 H-allele. The specification describes methods for typing
 CC alleles (preferably the H and R alleles) of the minor histocompatibility
 CC antigen HA-1 in a sample, which comprise detecting polymorphic
 CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
 CC methods can be used for HA-1 typing for bone marrow transplants, severe
 CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
 CC detection of genetic aberrances. The probes and primers of the invention
 CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
 CC anti-idiotypic B cells and/or T cells and antibodies
 XX SQ Sequence 9 AA;

Query Match 88.1%; Score 37; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VRDDLLRA 9
 |||||
 Db 1 VLHDDLLRA 9

RESULT 6
 ID ADH40333 standard; peptide; 9 AA.
 AC ADH40333;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Human minor histocompatibility antigen HA-1 T cell epitope.
 XX
 KM human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
 KM minor histocompatibility antigen; mAb; T cell epitope.
 XX
 OS Homo sapiens.
 XX
 PN WO2003106692-A2.
 XX
 PD 24-DEC-2003.
 XX
 PF 13-JUN-2003; 2003WO-EP006251.
 XX
 PR 13-JUN-2002; 2002EP-00013423.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Strittmatter W, Moll H;
 XX
 DR WPI; 2004-082200/08.

XX PT Providing allelic variant epitope of protein based on single nucleotide
 PT polymorphism by defining target protein, screening database of protein,
 PT identifying, selecting allelic variant protein, creating variant
 PT epitopes.
 XX
 XX Disclosure; Page 82; 119pp; English.

XX CC The invention relates to a novel method for providing epitopes of allelic
 CC variants of antigenic proteins from specific species based on single
 CC nucleotide polymorphism (SNP), by defining target protein/peptide or its
 CC subset, screening database of DNA encoding target protein, identifying,
 CC selecting allelic peptide/protein variants, expression product or its
 CC fragment encoded by DNA sequence having SNP, creating variant epitopes,
 CC selecting epitopes binding to MHC protein. A protein of the invention has
 CC cytostatic activity, and may have a use in a vaccine. The method is

CC useful for generating a SNP profile of one or more individuals from a
 CC given species by applying the method for several protein from the
 CC individuals, where the SNP profile was related to disease, preferably
 CC cancer. This is useful for diagnosing a disease in an individual by
 CC generating the SNP-related polymorphic profile. A method of the invention
 CC is useful for transplanting haematopoietic stem cells from a donor to a
 CC recipient and treating cancer, preferably leukaemia, and for determining
 CC the progression, regression or onset of a treated disease. The present
 CC sequence is used in the exemplification of the invention.

XX
 SQ Sequence 9 AA;

Query Match 88.1%; Score 37; DB 8; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 1;

Qy 1 VLRDDLLA 9
 1 VLHDDLLEA 9

Db

RESULT 7
 AAW9195 standard; peptide; 9 AA.

XX AAW9195;

DT 20-MAY-1999 (first entry)

XX Minor histocompatibility antigen HA-1 T-cell epitope #1.

XX Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
 KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
 KW diagnosis; aplastic anaemia; immune deficiency disease.

XX Homo sapiens.

OS Synthetic.

FT Key Location/Qualifiers

FT Misc-difference 3 /label= His, Arg

XX WO9905174-A1.

PD 04-FEB-1999.

XX 23-JUL-1998; 98WO-NL000425.

XX 23-JUL-1997; 97EP-00202303.

XX (UYLE-) RIJKSUNIV LEIDEN.

PI Goulmy EAJM, Hunt DF, Engelhard VH;

XX WPI; 1999-153312/13.

XX A new minor histocompatibility antigen, HA-1 - useful to treat immune
 PT diseases and prevent rejection and host versus graft disease in bone
 PT marrow and organ transplantation.

XX Claim 1; Page 32; 47pp; English.

XX The present sequence represents a new peptide (PI) constituting a T-cell
 CC epitope obtainable from the minor histocompatibility antigen HA-1. The
 CC peptide is immunogenic and can be used as part of a vaccine. PI is used
 CC as a medicine, to induce tolerance for transplants, prevent rejection
 CC and/or graft versus host disease, or to treat (auto) immune diseases. In
 CC particular it can be used with bone marrow transplantation, in the
 CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
 CC diseases

XX Sequence 9 AA;

Query Match 85.7%; Score 36; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 1;

Qy 1 VLRDDLLA 9
 1 VLHDDLLEA 9

Db

RESULT 8
 AAW97572 standard; peptide; 9 AA.

XX AAW97572;

DT 20-MAY-1999 (first entry)

XX T-cell epitope from the minor histocompatibility antigen HA-1.

XX T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
 KW transplant rejection; Graft-versus-Host Disease; autoimmune disease;
 KW neoplastic haematopoietic cell.

XX Homo sapiens.

FT Key Location/Qualifiers

FT Misc-difference 3 /note= "His or Arg"

XX WO9905173-A1.

PD 04-FEB-1999.

XX 23-JUL-1998; 98WO-NL000424.

XX 23-JUL-1997; 97EP-00202303.

XX (UYLE-) RIJKSUNIV LEIDEN.

PI Goulmy EAJM, Hunt DF, Engelhard VH;

XX WPI; 1999-142855/12.

XX Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
 PT for inducing tolerance to transplants and prevent rejection or graft-
 PT versus-host disease.

XX Claim 1; Page 39; 57pp; English.

XX The present sequence represents an immunogenic peptide constituting a T-
 CC cell epitope, obtainable from the minor histocompatibility antigen HA-1.
 CC The peptide can be used in vaccines or pharmaceutical formulations as
 CC medicines to induce tolerance for transplants so as to prevent rejection
 CC and/or Graft-versus-Host Disease, or to treat autoimmune diseases.
 CC Neoplastic haematopoietic cells presenting the peptides, in an HLA class
 CC I context, can be eliminated after specific recognition of the peptides.
 CC The peptides can also be used to raise antibodies, T-cell receptor, B-
 CC and T-cells

XX Sequence 9 AA;

Query Match 85.7%; Score 36; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 1;

Qy 1 VLRDDLLA 9
 1 VLHDDLLEA 9

Db

RESULT 9
 ADT73023 standard; peptide; 9 AA.

XX AC ADT73023;
XX 13-JAN-2005 (first entry)
XX DE Human RSV L high affinity binding peptide Segid 919.
XX DE human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
XX KM MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.
XX OS Human respiratory syncytial virus.
XX PN WO2004092207-A2.
XX PD 28-OCT-2004.
XX PF 16-APR-2004; 2004WO-EP004061.
XX PR 16-APR-2003; 2003BP-00447095.
XX PA (ALGO-) ALGONOMICS NV.
XX PI Lasters I, Desmet J, Stegmann T;
XX DR WPI; 2004-758334/74.
XX PT New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
XX PT or P) for inducing an immune response to RSV or for diagnosing,
XX PT preventing or treating viral infections, particularly RSV infection.
XX PS Claim 16; SEQ ID NO 919; 143pp; English.
XX XX
XX CC This invention relates to novel isolated or purified peptides of the
XX CC human respiratory syncytial virus (RSV), in particular ten RSV genes
XX CC encoding 11 separate viral proteins: non-structural proteins NS-1 (also
XX CC known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and
XX CC eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
XX CC SH (also known as the 1A protein). Specifically, it refers to a
XX CC composition comprising an above peptide mixed with a pharmaceutical
XX CC excipient or an RSV immunogenic composition comprising a recombinant
XX CC expression vector with a nucleic acid insert encoding an above peptide.
XX CC The present invention describes an in vitro method of detecting cytotoxic
XX CC T lymphocytes (CTLs) that respond to a major histocompatibility complex
XX CC (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
XX CC RSV peptide is useful for preparing a diagnostic composition or an RSV
XX CC (prophylactic or therapeutic) vaccine composition for a DNA-based
XX CC immunisation, or for preparing an immune response provoking vaccine in
XX CC the event of RSV infection (the vaccine being prepared by contacting the
XX CC polypeptide in an immune response-provoking amount of specific CTL).
XX CC Accordingly, these peptide compositions have virucidal activity. This
XX CC peptide sequence is a human RSV high binding affinity peptide of the
XX CC invention.
XX CC
XX SQ Sequence 9 AA;
XX
XX Query Match 69.0%; Score 29; DB 8; Length 9;
XX Best Local Similarity 44.4%; Pred. No. 2e+06;
XX Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 VLKDDLLLEA 9
XX :|||:|:
XX Db 1 IIKDILSLA 9
XX
XX RESULT 10
XX ID AAM47427 standard; peptide; 9 AA.
XX XX AAM47427;
XX AC AAM47427;
XX XX
XX DT 05-JUN-1998 (first entry)
XX XX
XX DE Prenyl diphosphate synthetase preserved region VI sequence.

XX XX
XX KM Prenyl diphosphate synthetase; polyprenyl diphosphate; vitamin K;
XX KM ubiquinone; preserved region VI.
XX OS Synthetic.
XX OS EP812914-A2.
XX PN EP812914-A2.
XX PD 17-DEC-1997.
XX PF 13-JUN-1997; 97EP-00109692.
XX PR 14-JUN-1996; 96JP-00154441.
XX XX (TOYT) TOYOTA JIDOSHA KK.
XX PA Muramatsu M, Koike A, Ogura K, Koyama T, Shimizu N, Cho Y;
XX PI WPI; 1998-034975/04.
XX DR
XX PT DNA encoding prenyl diphosphate synthetase subunit(s) - new Micrococcus
XX PT Prenyl diphosphate synthetase subunit polypeptide(s), and methods for
XX PT preparing enzymes from subunit(s).
XX PS Example 2; Page 26; 46pp; English.
XX XX
XX CC The present sequence from preserved region VI of prenyl diphosphate
XX CC synthetase (PDS), was used in the preparation of primers for the
XX CC amplification of PDS DNA. Substances synthesised by PDS, i.e. polyprenyl
XX CC diphosphates, are precursors of physiologically active substances, e.g.
XX CC vitamin K and ubiquinones
XX CC
XX SQ Sequence 9 AA;
XX
XX Query Match 64.3%; Score 27; DB 2; Length 9;
XX Best Local Similarity 57.1%; Pred. No. 2e+06;
XX Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 LKDDLLLE 8
XX :|||:|:
XX Db 3 IRDDILD 9
XX
XX RESULT 11
XX ADT73690
XX ID ADT73690 standard; peptide; 9 AA.
XX XX
XX AC ADT73690;
XX XX
XX DT 13-JUN-2005 (first entry)
XX XX
XX DE Human RSV L high affinity binding peptide Segid 1586.
XX XX
XX KM human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
XX KM MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.
XX OS Human respiratory syncytial virus.
XX PN WO2004092207-A2.
XX PD 28-OCT-2004.
XX PF 16-APR-2004; 2004WO-EP004061.
XX PR 16-APR-2003; 2003BP-00447095.
XX PA (ALGO-) ALGONOMICS NV.
XX PI Lasters I, Desmet J, Stegmann T;
XX DR WPI; 2004-758334/74.
XX PT New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N

PT or P) for inducing an immune response to RSV or for diagnosing, preventing or treating viral infections, particularly RSV infection.

CC human respiratory syncytial virus (RSV), in particular ten RSV genes
CC encoding 11 separate viral proteins: non-structural proteins NS-1 (a
CC known as the 1C protein) & NS-2 (1B protein), a polymerase protein L
CC eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, M2-3

This invention relates to novel isolated or purified peptides of the human respiratory syncytial virus (RSV), in particular ten RSV genes encoding 11 separate viral proteins: non-structural proteins NS-1 (also known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and SH (also known as the 1A protein). Specifically, it refers to a composition comprising an above peptide mixed with a pharmaceutical excipient or an RSV immunogenic composition comprising a recombinant expression vector with a nucleic acid insert encoding an above peptide. The present invention describes an in vitro method of detecting cytooxidase T lymphocytes (CTLs) that respond to a major histocompatibility complex (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The RSV peptide is useful for preparing a diagnostic composition or an RSV (propylactic or therapeutic) vaccine composition for a DNA-based immunisation, or for preparing an immune response provoking vaccine in the event of RSV infection (the vaccine being prepared by contacting the polypeptide in an immune response-provoking amount of specific CTL). Accordingly, these peptide compositions have virucidal activity. This peptide sequence is a human RSV high binding affinity peptide of the invention.

Sequence 9 AA;

Query Match	61.9%;	Score 26;	DB 8;	Length 9;
Best Local Similarity	44.4%;	Pred. No. 2e+06;		
Matches 4; Conservative	4;	Mismatches	0;	Gaps 0;

```
QY      1 VRDDELEA 9
        ::::|::|
Db      1 IKODILEA 9
```

RESULT 12
ADT72767
ID ADT72767 standard; peptide: 9 AA

AC	ADT72767;
XX	
DT	13-JAN-2005 (first entry)

DE Human RSV L high affinity binding peptide SeqID 663.

KM human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine
KW

OS Human respiratory syncytial virus.

PN WO2004092207-A2.

PD 28-OCT-2004.

PF 16-APR-2004; 2004WO-EP004061.

PR 16-APR-2003; 2003EP-00447095.

PA (ALGO-) ALGONOMICS NV.

PI Lasters I, Desmet J, Stegmann T;

DR WPI; 2004-758334/74.

PT New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N or P) for inducing an immune response to RSV or for diagnosing, preventing or treating viral infections, particularly RSV infection.

PS Disclosure; SEQ ID NO 663; 143bp; English.

CC This invention relates to novel isolated or purified peptides of the

human respiratory syncytial virus (RSV), in particular ten RSV genes encoding 11 separate viral proteins: non-structural proteins NS-1 (also known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and SH (also known as the 1A protein). Specifically, it refers to a composition comprising an above peptide mixed with a pharmaceutical expellant or an RSV immunogenic composition comprising a recombinant expression vector with a nucleic acid insert encoding an above peptide. The present invention describes an in vitro method of detecting cytotoxic T lymphocytes (CTLs) that respond to a major histocompatibility complex (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The RSV peptide is useful for preparing a diagnostic composition or an RSV (prophylactic or therapeutic) vaccine composition for a DNA-based immunization, or for preparing an immune response provoking vaccine in the event of RSV infection (the vaccine being prepared by contacting the polypeptide in an immune response-provoking amount of specific CTL). Accordingly, these peptide compositions have virucidal activity. This peptide sequence is a human RSV high binding affinity peptide of the invention.

Sequence 9 AA:

Query Match	61.9%;	Score 26;	DB 8;	Length 9;
Best Local Similarity	50.0%;	Pred. No. 2e+06;		
Matches 4; Conservative	3;	Mismatches	1;	Indels 0;
				Gaps 0

QY	2	LRDDLEA	9
		::: :	
Db	1	IKDDLSA	8

RESULT 13
AAU71428
ID AAU71428 standard; peptide; 9 AA

AC AAU71428;

DT 26-FEB-2002 (first entry)

Human MHC molecule HLA-A11 binding 103P3E8 peptide #35.

AA
KM
KM
KM
KM
KM
KM

103P5E8; prostate; bladder; kidney; colon; lung; breast; rectum; stomach;
tumor; cancer; cytostatic; gene therapy; antibody therapy; ribozyme;
single chain monoclonal antibody; serum; blood; urine; tissue; human;
chromosome 9q13-q21.

Homo sapiens.

PN W0200179557-A2.

PD 25-OCT-2001

PF 12-APR-2001; 2001WO-US012181

12-APR-2000; 2000US-0196647P.

PA (UROG-) UROGENESYS INC.

PI Faris M, Challita-Eid PM, Raitano AB, Mitchell SC, Afar DEH;

PI Jakobovits

DR WPI; 2002-061976/08.

PT Monitoring 103P3B8 gene products in sample from patient (suspected of
PT having cancer, useful for diagnosing, managing or treating cancers, e.g.,
PT prostate cancer, comprises determining presence of aberrant 103P3B8 gene
PT products.

PS Disclosure; Page 90; 128pp; English

CC Sequences AAU10193-AAU71796 represent the 103P3E8-related protein and CC peptide fragments of the protein. 103P38 exhibits tissue specific CC expression in normal adult tissue, but it is also aberrantly expressed in

CC many cancers including tumours of the prostate, bladder, kidney, colon,
CC lung, breast, rectum and stomach. The 103P3B8 polynucleotide, its related
CC protein and peptide fragments and specific PCR primers are therefore
CC useful for diagnosing and treating cancer. A vector comprising a
CC polynucleotide which encodes a single chain monoclonal antibody, that
CC immunospecifically binds to an 103P3B8-related protein, and a ribozyme
CC capable of cleaving a polynucleotide having the 103P3B8 coding sequence,
CC are both useful in the preparation of a composition for treating a
CC patient with a cancer that expresses 103P3B8. The sequences can be used
CC in diagnostic methods to monitor the level of 103P3B8 gene products in
CC serum, blood, urine and tissue and to thereby detect the presence of
CC cancerous cells

SQ Sequence 9 AA;

Query Match 59.5%; Score 25; DB 5; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 LRDDLLA 9
:::|||||
DB 2 VKDDLLEA 9

RESULT 14

ADT72766 standard; peptide; 9 AA.

ADT72766;

13-JAN-2005 (first entry)

Human RSV L high affinity binding peptide SeqID 662.

human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.

Human respiratory syncytial virus.

WO2004092207-A2.

28-OCT-2004.

16-APR-2004; 2004WO-EP004061.

16-APR-2003; 2003EP-00447095.

(ALGO-) ALGONOMICS NV.

Laetters I, Desmet J, Stegmann T;

WPI; 2004-758334/74.

New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
or P) for inducing an immune response to RSV or for diagnosing,
preventing or treating viral infections, particularly RSV infection.
Disclosure; SEQ ID NO 662, 143pp, English.

This invention relates to novel isolated or purified peptides of the
human respiratory syncytial virus (RSV), in particular ten RSV genes
encoding 11 separate viral proteins: non-structural proteins NS-1 (also
known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and
eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
SH (also known as the 1A protein). Specifically, it refers to a
composition comprising an above peptide mixed with a pharmaceutical
excipient or an RSV immunogenic composition comprising a recombinant
expression vector with a nucleic acid insert encoding an above peptide.
The present invention describes an in vitro method of detecting cytotoxic
T lymphocytes (CTLs) that respond to a major histocompatibility complex
(MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
RSV peptide is useful for preparing a diagnostic composition or an RSV
(propylactic or therapeutic) vaccine composition for a DNA-based

CC immunisation, or for preparing an immune response provoking vaccine in
CC the event of RSV infection (the vaccine being prepared by contacting the
CC polypeptide in an immune response-provoking amount of specific CTL).
CC Accordingly, these peptide compositions have virucidal activity. This
CC peptide sequence is a human RSV high binding affinity peptide of the
CC invention.

SQ Sequence 9 AA;

Query Match 59.5%; Score 25; DB 8; Length 9;
Best Local Similarity 42.9%; Pred. No. 2e+06;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLDDLL 7
:::|||||
DB 2 IIKDDL 8

RESULT 15

ADT73689 standard; peptide; 9 AA.

ADT73689;

13-JAN-2005 (first entry)

Human RSV L high affinity binding peptide SeqID 1585.

human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.

Human respiratory syncytial virus.

WO2004092207-A2.

28-OCT-2004.

16-APR-2004; 2004WO-EP004061.

16-APR-2003; 2003EP-00447095.

(ALGO-) ALGONOMICS NV.

Laetters I, Desmet J, Stegmann T;

WPI; 2004-758334/74.

New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
or P) for inducing an immune response to RSV or for diagnosing,
preventing or treating viral infections, particularly RSV infection.
Claim 16; SEQ ID NO 1585; 143pp; English.

This invention relates to novel isolated or purified peptides of the
human respiratory syncytial virus (RSV), in particular ten RSV genes
encoding 11 separate viral proteins: non-structural proteins NS-1 (also
known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and
eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
SH (also known as the 1A protein). Specifically, it refers to a
composition comprising an above peptide mixed with a pharmaceutical
excipient or an RSV immunogenic composition comprising a recombinant
expression vector with a nucleic acid insert encoding an above peptide.
The present invention describes an in vitro method of detecting cytotoxic
T lymphocytes (CTLs) that respond to a major histocompatibility complex
(MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
RSV peptide is useful for preparing a diagnostic composition or an RSV
(propylactic or therapeutic) vaccine composition for a DNA-based
immunisation, or for preparing an immune response provoking vaccine in
the event of RSV infection (the vaccine being prepared by contacting the
polypeptide in an immune response-provoking amount of specific CTL).
Accordingly, these peptide compositions have virucidal activity. This
peptide sequence is a human RSV high binding affinity peptide of the
invention.

XX Sequence 9 AA;

Query Match 59.5%; Score 25; DB 8; Length 9;
 Best Local Similarity 42.9%; Pred. No. 2e+06;
 Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLKDDLL 7
 ::|||:
 Db 2 IIKDDIL 8

Search completed: April 6, 2006, 16:19:10
 Job time : 112.667 secs

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: April 6, 2006, 16:19:36 ; Search time 18.6667 Seconds
(without alignments)
46.390 Million cell updates/sec

Title: US-10-791-217A-5

Perfect score: 42
Sequence: 1 VLRDDLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38.1	7	2	S68004	hucolin, 75K chain
2	38.1	8	2	PC4131	hypothetical prote
3	35.7	7	2	A59489	protein kinase C 1
4	33.3	7	2	S20446	elastase - Pseudom
5	33.3	9	2	A60427	macrophage cytolox
6	31.0	9	2	PH0942	T-cell receptor be
7	28.6	4	2	I40697	biotin A - Citruba
8	28.6	5	2	PT0679	T-cell receptor be
9	28.6	5	2	PT0601	T-cell receptor be
10	28.6	6	2	B35640	cerbellar degener
11	28.6	6	2	PT0533	T-cell receptor be
12	28.6	7	2	A34026	acetylcholinestera
13	28.6	7	2	B39040	caldesquestrin, fas
14	28.6	7	2	PT0628	T-cell receptor be
15	28.6	7	2	PT0722	T-cell receptor be
16	28.6	7	2	PT0576	T-cell receptor be
17	28.6	8	2	PT0557	T-cell receptor be
18	28.6	8	2	A61328	tryptin (EC 3.4.21
19	28.6	9	2	PH0108	late Gl-69 protein
20	28.6	9	2	PT0562	T-cell receptor be
21	28.6	9	2	B30572	T-cell receptor be
22	28.6	9	2	A39841	sucrose 3-glucosyl
23	28.6	9	2	A37027	macrophage chemot
24	26.2	6	2	D60274	major protein anti
25	26.2	6	2	T11779	phosphoglycerate t
26	26.2	7	2	S25266	p1B protein - Esc
27	26.2	7	2	PT0602	T-cell receptor be
28	26.2	8	2	S22428	chitin-binding pro
29	26.2	8	2	B33099	158K exoantigen -

30	11	26.2	8	2	S69165	ferredoxin a2 - Ja
31	11	26.2	9	2	S66419	tetrameric protein
32	11	26.2	9	2	B28495	conopressin S - co
33	11	26.2	9	2	PH0002	chlorophyll a/b-b1
34	11	26.2	9	2	B39841	dextranucrase (EC
35	11	26.2	9	2	PS0253	glycine cleavage s
36	11	26.2	9	2	A12872	transaldolase (EC
37	11	26.2	9	2	B57444	neuropeptide Grb-A
38	11	26.2	9	2	C57444	neuropeptide Grb-A
39	11	26.2	9	2	A44787	callitricinamide 10
40	11	23.8	4	2	A48360	gamma subunit of p
41	10	23.8	4	2	A26209	protein-glutamine
42	10	23.8	4	2	A35779	neuropeptide Antho
43	10	23.8	6	2	B44510	hypothetical prote
44	10	23.8	6	2	H48394	glycoprotein compo
45	10	23.8	7	2	S78024	ribosomal protein

ALIGNMENTS

RESULT 1

S68004 hucolin, 75K chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C/Accession: S68004
R:Edgar, P.F.
FEBS Lett. 375, 159-161, 1995
A>Title: Hucolin, a new corticosteroid-binding protein from human plasma with structural
A/Reference number: S68004; PMID:96087107; PMID:7498469
A/Accession: S68004
A>Status: preliminary
A/Molecule type: protein
A/Residues: 1-7 <EDG>
A/Cross-references: UNIPARC:UPI000017C164

Query Match

Best Local Similarity 38.1%; Score 16; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0;

Qy 4 DDL 6
Db 4 DDL 6

RESULT 2

PC4131 hypothetical protein 8 (imported) - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004
C/Accession: PC4131
R:Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.
Gene 167, 87-91, 1995
A>Title: Sequencing and characterization of the downstream region of the genes encoding
Y for biohydrolysis of heme d1.
A/Reference number: J04552; PMID:96144254; PMID:8566817
A/Accession: PC4131
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-8 <KAW>
A/Cross-references: UNIPROT:P95412; UNIPARC:UPI000017A96A; DDBJ:D50473; NID:91217594
A/Note: this ORF is not annotated in GenBank entry PSENTRC, release 113.0
C/Superfamily: Pseudomonas stutzeri n1pD protein

Query Match

Best Local Similarity 38.1%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0;

Qy 4 DDL 6
Db 2 DDL 4

RESULT 3
 AS9489
 protein kinase C inhibitor - rat (fragment)
 C:Species: Rattus norvegicus
 C:Date: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 25-Aug-2003
 C:Accession: AS9489
 R:Negoro, M.
 Submitted to the Protein Sequence Database, June 2003
 A:Description: Purification of PKC1 from rat liver.
 A:Reference number: AS9489
 A:Accession: AS9489
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <NEG>
 A:Experimental source: strain Matar, liver
 A>Note: p-Hydroxyacetophenone-Sepharose binding protein

Query Match 35.7%; Score 15; DB 2; Length 7;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLKDD 5
 : ||
 Db 2 IFEDD 6

RESULT 4
 S20446
 elastase - Pseudomonas aeruginosa
 C:Species: Pseudomonas aeruginosa
 C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
 C:Accession: S20446
 R:Kessler, E.; Saitin, M.; Buretein, Y.
 FEBS Lett. 299, 291-293, 1992
 A:Title: Identification of cleavage sites involved in proteolytic processing of Pseudomonas
 A:Reference number: S20446; MUID:92183956; PMID:1544509
 C:Accession: S20446
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <KES>
 A:Cross-references: UNIPARC:UPI000017A95F

Query Match 33.3%; Score 14; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 DLLE 8
 : ||:
 Db 3 DLID 6

RESULT 5
 A60427
 macrophage cytotoxicity-inducing factor, 29k - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
 C:Accession: A60427
 R:Jones, C.M.; Prince, C.A.; Williams, J.S.
 Exp. Hematol. 19, 704-709, 1991
 A:Title: Purification and amino acid analysis of a human macrophage cytotoxicity-inducin
 A:Reference number: A60427; MUID:91372335; PMID:1909970
 A:Accession: A60427
 A:Molecule type: protein
 A:Residues: 1-9 <JON>
 A:Cross-references: UNIPROT:Q7M4R5; UNIPARC:UPI0000142BE0
 A>Note: the sequence from the text on page 706 is inconsistent with that from page 708
 C:Keywords: cytokine

Query Match 33.3%; Score 14; DB 2; Length 9;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLKDD 4
 : ||
 Db 4 VLKDD 7

RESULT 6
 PH0942
 T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 C:Accession: PH0942
 R:Gold, D.P.; Ofiner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
 J. Exp. Med. 174, 1467-1476, 1991
 A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
 A:Reference number: PH0891; MUID:92078857; PMID:1835012
 A:Accession: PH0942
 A:Molecule type: mRNA
 A:Residues: 1-9 <GOL>
 A:Cross-references: UNIPARC:UPI000017C9DD
 A:Experimental source: complete Freund's adjuvant-immunized lymph node
 A>Note: the authors translated the codon TGC for residue 2 as Ala
 C:Keywords: T-cell receptor

Query Match 31.0%; Score 13; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LLR 8
 : ||
 Db 5 LLR 7

RESULT 7
 I40697
 biotin A - Citrobacter freundii (fragment)
 C:Species: Citrobacter freundii
 C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
 C:Accession: I40697
 R:Shian, D.; Campbell, A.
 Gene 67, 203-211, 1988
 A:Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter
 A:Reference number: I40697; MUID:89006280; PMID:2971595
 A:Accession: I40697
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-4 <RES>
 A:Cross-references: UNIPROT:P13071; UNIPARC:UPI000017AA21; GB:M21922; NID:g144434

Query Match 28.6%; Score 12; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 5
 : ||
 Db 3 DD 4

RESULT 8
 PT0679
 T-cell receptor beta chain V-D-J region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0679; P10708
 R:Feeney, A.U.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:9127601; PMID:1711558
 A:Accession: PT0679
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-5 <FEF>
 A:Cross-references: UNIPARC:UPI000017C84D
 A:Experimental source: day 18 fetal thymus, strain BALB/c, 154-2J

A:Accession: PT0708
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <FE2>
A:Cross-references: UNIPARC:UPI000017C84D
A:Experimental source: newborn thymus, strain BALB/c, 161-2B
C:Keywords: T-cell receptor

Query Match 28.6%; Score 12; DB 2; Length 5;
Best local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 5
DB 4 DD 5

RESULT 9
PT0601
T-cell receptor beta chain V-D-J region (120-2K) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: PT0601; PT0694
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; PMID:91277601; PMID:1711558
A:Accession: PT0601
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE2>
A:Cross-references: UNIPARC:UPI000017C7B6
A:Experimental source: newborn thymus, strain BALB/c, clone 120-2K
A:Accession: PT0617
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE3>
A:Cross-references: UNIPARC:UPI000017C7B6
A:Experimental source: newborn thymus, strain BALB/c, 120-2CA
A:Accession: PT0694
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <FE2>
A:Cross-references: UNIPARC:UPI000017C7B6
A:Experimental source: day 18 fetal thymus, strain BALB/c, 154-1H
C:Keywords: T-cell receptor

Query Match 28.6%; Score 12; DB 2; Length 5;
Best local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 5
DB 4 DD 5

RESULT 10
B35640
cerebellar degeneration-related protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 24-Jun-1993
C:Accession: B35640
R:Chen, Y.T.; Rettig, W.J.; Yanamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, J.H.
Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990
A:Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal marker
A:Reference number: A35640; PMID:90222173; PMID:2326268
A:Accession: B35640
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-6 <CHE>
A:Cross-references: UNIPARC:UPI000017C63A

Query Match 28.6%; Score 12; DB 2; Length 6;

Best local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 6
DB 3 EDL 5

RESULT 11
PT0533
T-cell receptor beta chain V-D-J region (126-1AA) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0533
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; PMID:91277601; PMID:1711558
A:Accession: PT0533
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FE2>
A:Cross-references: UNIPARC:UPI000017C801
A:Experimental source: adult thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 28.6%; Score 12; DB 2; Length 6;
Best local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 5
DB 4 DD 5

RESULT 12
A34026
acetylcholinesterase (RC 3.1.1.7) 5.6S form - Pacific electric ray (fragment)
C:Species: Torpedo californica (Pacific electric ray)
C>Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 08-Nov-1996
C:Accession: A34026
R:Gibney, G.; MacPhee-Quigley, K.; Thompson, B.; Vedvick, T.; Low, M.G.; Taylor, S.S.;
J. Biol. Chem. 263, 1140-1145, 1988
A:Title: Divergence in primary structure between the molecular forms of acetylcholinesterase
A:Reference number: A34026; PMID:8807239; PMID:333534
A:Accession: A34026
A:Molecule type: protein
A:Residues: 1-7 <GIB>
A:Cross-references: UNIPARC:UPI000017BF32
C:Keywords: alternative splicing; carboxylic ester hydrolase

Query Match 28.6%; Score 12; DB 2; Length 7;
Best local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 LLEA 9
DB 1 LLNA 4

RESULT 13
B39040
caseinoglycin, fast skeletal muscle - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
C:Accession: B39040
R:Calaf, S.E.; Jones, L.R.
J. Biol. Chem. 266, 391-398, 1991
A:Title: Phosphorylation of cardiac and skeletal muscle caseinoglycin isoforms by casein
A:Reference number: A39040; PMID:91093153; PMID:1985907
A:Accession: B39040
A:Status: preliminary
A:Molecule type: protein

A:Residues: 1-7 <CAL>
 A:Cross-references: UNIPARC:UPI000017C5BC
 C:Keywords: phosphoprotein; skeletal muscle

Query Match 28.6%; Score 12; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 4 DD 5
 ||
 Db 1 DD 2

RESULT 14

PT0628
 T-cell receptor beta chain V-D-J region (111-1AG) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0628
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A>Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PF0509; MWID:91277601; PMID:1711558
 A:Accession: PT0628
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-7 <FEE>
 A:Cross-references: UNIPARC:UPI000017C7CD
 A:Experimental source: newborn thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 28.6%; Score 12; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 4 DD 5
 ||
 Db 4 DD 5

RESULT 15

PT0722
 T-cell receptor beta chain V-D-J region (135-1G) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0722
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A>Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MWID:91277601; PMID:1711558
 A:Accession: PT0722
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-7 <FEE>
 A:Cross-references: UNIPARC:UPI000017C81F
 A:Experimental source: newborn thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 28.6%; Score 12; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 4 DD 5
 ||
 Db 4 DD 5

Search completed: April 6, 2006, 16:26:10
 Job time: 18.6667 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 6, 2006, 16:13:46 ; Search time 118 Seconds

(without alignments)
53.811 Million cell updates/sec

Title: US-10-791-217A-5

Perfect score: 42

Sequence: 1 VLRLDLRA 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 1766

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_05.80:*

2: uniprot_sprot:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	42.9	8	2	Q7XB03_MAIZE
2	18	42.9	8	2	Q7XB07_MAIZE
3	16	38.1	9	2	Q7OSM2_HUMAN
4	16	38.1	9	2	Q7KYP6_HUMAN
5	16	38.1	9	2	Q8LPT5_MAIZE
6	16	38.1	9	2	P82568_STRPY
7	15	35.7	8	2	P72279_RHOC
8	15	35.7	8	2	Q80H91_PPRA
9	15	35.7	9	2	Q9UR26_HUMAN
10	15	35.7	9	2	Q9XJN0_VVIRU
11	15	35.7	9	2	Q4QWV3_9MARC
12	15	35.7	9	2	Q4QWV9_9MARC
13	15	35.7	9	2	P83539_LACSN
14	15	35.7	8	2	Q51594_9Z22Z
15	14	33.3	8	2	Q8KPK4_9CHRO
16	14	33.3	8	2	Q921B9_NEIME
17	14	33.3	9	2	Q7M4R5_HUMAN
18	14	33.3	9	2	Q9F8Z2_CICAR
19	14	33.3	9	2	Q563E0_9CYAN
20	14	33.3	9	2	Q9QZAB_MOUSE
21	14	33.3	9	2	Q6Q7G0_RARRI
22	14	33.3	9	2	Q85710_9RETR
23	14	33.3	9	2	Q8UTD7_9HIV1
24	13	31.0	7	2	Q15897_HUMAN
25	13	31.0	8	2	Q9HDS4_ASPPL
26	13	31.0	8	2	Q5RSL1_PIG
27	13	31.0	8	2	Q6UC68_SOYBN
28	13	31.0	8	2	Q93SR0_STAP
29	13	31.0	8	2	Q9QVJ8_9MURI
30	13	31.0	8	2	Q89965_POVJC
31	13	31.0	8	2	Q6PUD5_SV40

32	13	31.0	8	2	Q6PUD7_SV40	Q6PUD7 simian viru
33	13	31.0	8	2	Q6PUD9_SV40	Q6PUD9 simian viru
34	13	31.0	8	2	Q6PUB1_SV40	Q6PUB1 simian viru
35	13	31.0	8	2	Q6QSK9_SV40	Q6QSK9 simian viru
36	13	31.0	8	2	Q64IX4_FUNHE	Q64IX4 fundulus he
37	13	31.0	9	1	IPYR_RHOVI	P82992 rhodopseudo
38	13	31.0	9	2	Q7RYB9_NEUCR	Q7RYB9 neurospora
39	13	31.0	9	2	Q6LCV2_HUMAN	Q6LCV2 homo sapien
40	13	31.0	9	2	Q6UYK2_MALDO	Q6UYK2 malus domes
41	13	31.0	9	2	Q568S9_SAMCA	Q568S9 sambucus ca
42	13	31.0	9	2	Q568T0_9DIPS	Q568T0 viburnum ur
43	13	31.0	9	2	Q568T1_9DIPS	Q568T1 viburnum ur
44	13	31.0	9	2	Q568T2_9DIPS	Q568T2 viburnum tr
45	13	31.0	9	2	Q568T3_VIBOP	Q568T3 viburnum op

ALIGNMENTS

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RESULT 1
Q7XB03_MAIZE
ID Q7XB03_MAIZE PRELIMINARY; PRT; 8 AA.
AC Q7XB03;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Phytoene synthase 2 (Fragment).
GN Name=psyl2;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Y-3;
RX MEDLINE=22779048; PubMed=12897253; DOI=10.1105/tpc.012526;
RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;
RT "Contrasting effects of selection on sequence diversity and linkage
disequilibrium at two phytoene synthase loci.";
RL Plant Cell 15:1795-1806(2003).
DR EMBL; AY300612; AAP55351.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 8
FT SEQUENCE 8 AA; 915 MW; 5D1862CAB4072054 CRC64;
SQ
Query Match 42.9%; Score 18; DB 2; Length 8;
Best local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLRLD 4
Db 2 ILRD 5
RESULT 2
Q7XB07_MAIZE
ID Q7XB07_MAIZE PRELIMINARY; PRT; 9 AA.
AC Q7XB07;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-FEB-2005 (TEMBLrel. 29, Last annotation update)
DE Phytoene synthase 2 (Fragment).
GN Name=psyl2;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Y-13, and W-16;
RX MEDLINE=22779048; PubMed=12897253; DOI=10.1105/tpc.012526;
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RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;
RT "Contrasting effects of selection on sequence diversity and linkage
RL disequilibrium at two phytoene synthase loci.";
RL Plant Cell 15:1795-1806(2003).
DR EMBL; AY300641; AAP55379.1; -; Genomic_DNA.
DR EMBL; AY300665; AAP55403.1; -; Genomic_DNA.
FT NON_TER 1
RT NON_TER 1
SQ SEQUENCE 9 AA; 1016 MW; 1D1C62CAB4072054 CRC64;

Query Match
Best Local Similarity 42.9%; Score 18; DB 2; Length 9;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLRD 4
   |||
Db 3 ILRD 6

RESULT 3
Q70SM2_HUMAN
ID Q70SM2_HUMAN PRELIMINARY; PRT; 9 AA.
AC Q70SM2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypermethylated in cancer 1 (Fragment).
GN Name=HIC1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RA Pine S. Guerardel C., Deltour S., Godwin A.K., Lepince D.;
RT "Identification of a second G-C-rich promoter conserved in the human,
RL murine and rat tumor suppressor genes HIC1."
DR EMBL; AJ550616; CAD79467.1; -; mRNA.
FT NON_TER 9
SQ SEQUENCE 9 AA; 964 MW; 5B5E6DD1681AA7 CRC64;

Query Match
Best Local Similarity 38.1%; Score 16; DB 2; Length 9;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DLLEA 9
   |||
Db 3 DTMEA 7

RESULT 4
Q7KYP6_HUMAN
ID Q7KYP6_HUMAN PRELIMINARY; PRT; 9 AA.
AC Q7KYP6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE M4.V glycoprotein (exon P3B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Milkteiberger class V;
RA MEDLINE=90005483; PubMed=2792104;
RA Vignal A., Rahuel C., El-Maliki B., London J., Le Vankim C.,
RA Blanchard C.D.;
RT "Molecular Analysis of glycophorin A and B gene structure and

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RT expression . . . .";
RL Eur. J. Biochem. 184:337-344(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Milkteiberger class V;
RA Vignal A., Rahuel C., El-Maliki B., London J., Le Vankim C.,
RA Blanchard C.D.;
RT "Molecular Analysis of glycophorin A and B gene structure and
RT expression . . . .";
RL Eur. J. Biochem. 184:0-0(1989).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Milkteiberger class V;
RA Cartron J.P.;
RT Submitted (JUL-1989) to the EMBL/Genbank/DBJ databases.
DR EMBL; X15824; CAA33822.1; -; Genomic_DNA.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1073 MW; 50D145B7244AB403 CRC64;

Query Match
Best Local Similarity 38.1%; Score 16; DB 2; Length 9;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RDDL 6
   |||
Db 3 RDNL 6

RESULT 5
Q8LPT5_MAIZE
ID Q8LPT5_MAIZE PRELIMINARY; PRT; 9 AA.
AC Q8LPT5;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Beta-expansin-like protein (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
RA Morgante M., Rafalski J.A.; EMBL/Genbank/DBJ databases.
RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF094310; AAM21836.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 9 AA; 977 MW; 5C05B2D2CB1AA3 CRC64;

Query Match
Best Local Similarity 38.1%; Score 16; DB 2; Length 9;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLRA 9
   ||::|
Db 4 DEVYDA 9

RESULT 6
P82568_STRPY
ID P82568_STRPY PRELIMINARY; PRT; 9 AA.
AC P82568;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.

```

RC STRAIN=GRS4;
 RA Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
 RA Vanogegelen R.A.;
 RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
 RT proteins";
 RL Submitted (MAY-2000) to Swiss-Prot.
 CC -1- MASS SPECTROMETRY: MW=22592.04; METHOD=Electrospray.
 FT NON TER 1 1
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1069 MW; 2A771042CB1AB2D7 CRC64;

Query Match 38.1%; Score 16; DB 2; Length 9;
 Best Local Similarity 40.0%; Pred. No. 2.2e+06;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8
 Db 4 DEVIE 8

RESULT 7
 P72279 RHOCQ PRELIMINARY; PRT; 8 AA.
 ID F72279_RHOCQ PRELIMINARY; PRT; 8 AA.
 AC P72279;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Biphenyl dioxygenase (Fragment).
 GN Name=bphB;
 OS Rhodococcus globerulus.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Nocardiaceae; Rhodococcus.
 OC NCBI_Taxid=33008;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=95255652; PubMed=7737502; DOI=10.1016/0378-1119(94)00530-6;
 RA Asturias J.A., Diaz E., Timms K.N.;
 RT "Evolutionary relationship of the biphenyl dioxygenase of the gram-
 RT positive bacterium Rhodococcus globerulus P6 to multicomponent
 RT dioxygenase of gram-negative bacteria";
 RL Gene 156:11-18(1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Asturias J.;
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X80041; CAA56350.1; -; Genomic DNA.
 DR GO; GO:0016702; Foxidoreductase activity, acting on single d. . .; IEA.
 KW Dioxygenase.
 FT NON TER 8 8
 FT NON TER 9 9
 SQ SEQUENCE 8 AA; 989 MW; EBD2CB1AB6D73406 CRC64;

Query Match 35.7%; Score 15; DB 2; Length 8;
 Best Local Similarity 33.3%; Pred. No. 2.2e+06;
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 LDDLL 7
 Db 3 LQDEV 8

RESULT 8
 O80H91_9PARA PRELIMINARY; PRT; 8 AA.
 ID O80H91_9PARA PRELIMINARY; PRT; 8 AA.
 AC O80H91;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE HN/HNO (Fragment).
 GN Name=HN/HNO;
 OS Newcastle disease virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Avulaviruses.
 OC NCBI_Taxid=11176;

RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=94175786; PubMed=8129624;
 RA Collins M.S., Strong I., Alexander D.D.;
 RT "Evaluation of the molecular basis of pathogenicity of the variant
 RT Newcastle disease viruses termed 'pigeon PMV-1 viruses';"
 RL Arch. Virol. 134:403-411(1994).
 DR EMBL; S69419; AAP19628.1; -; Genomic DNA.
 FT NON TER 1 1
 FT NON TER 1 1
 SQ SEQUENCE 8 AA; 929 MW; 33D4087AA337205B CRC64;

Query Match 35.7%; Score 15; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.2e+06;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLKD 4
 Db 2 ILKD 5

RESULT 9
 Q9UE26_HUMAN
 ID Q9UE26_HUMAN PRELIMINARY; PRT; 9 AA.
 AC Q9UE26;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PEG1/MEST Protein.
 GN Name=PEG1/MEST;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=97336048; PubMed=9192843; DOI=10.1006/geno.1997.4731;
 RA Riesewijk A.M., Hu L., Schulz U., Tariverdian G., Hoeglund P.,
 RA Kere J., Ropers H.H., Kaltschauer V.M.;
 RT "Monoclonal expression of human PEG1/MEST is paralleled by parent-
 RT specific methylation in fetuses";
 RL Genomics 42:236-244(1997).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Kaltschauer V.M.M.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y10620; CAA71631.1; -; Genomic DNA.
 DR GO; GO:0016787; F.hydrolase activity; NAS.
 SQ SEQUENCE 9 AA; 1258 MW; C52D07340AB41412 CRC64;

Query Match 35.7%; Score 15; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLKDL 6
 Db 2 VLKDL 7

RESULT 10
 Q9XJN0_GVIRU PRELIMINARY; PRT; 9 AA.
 ID Q9XJN0_GVIRU PRELIMINARY; PRT; 9 AA.
 AC Q9XJN0;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE P10 (Fragment).
 GN Bacteriophage phi-10.
 OC Viruses; dsRNA viruses; Cystoviridae; Cystovirus.
 OC NCBI_Taxid=90889;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99350412; PubMed=10419946;

RA Minich L., Qiao X., Qiao J., Onodera S., Romantschuk M.,
 RA Hoogstraaten D., Isolation of additional bacteriophages with genomes of segmented
 RT double-stranded RNA.";
 RL J. Bacteriol. 181:4505-4508(1999).
 DR EMBL; AF125675; AAD22555.1; -; Genomic_RNA.
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1058 MW; 880B376AA720544A CRC64;

Query Match 35.7%; Score 15; DB 2; Length 9;
 Best Local Similarity 40.0%; Pred. No. 2.2e+06;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 8
 DB 2 DMLD 6

RESULT 11
 Q4QWV3_9MARC PRELIMINARY; PRT; 9 AA.
 ID Q4QWV3_9MARC PRELIMINARY; PRT; 9 AA.
 AC Q4QWV3;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE AtPB (Fragment).
 GN Name=atPB;
 OS Pallavicinia rubristipa.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
 OC Jungermanniopsida; Metzgeriales; Pallaviciniaceae;
 OC Pallaviciniaceae; Pallavicinia.
 OC NCBI_TaxId=280539;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Forrest L.L., Schutte S.W., Crandall-Stotler B.J., Stotler R.E.;
 RT "A Molecular Study of the Simple Thalloid Liverwort *Jensenia*
 (Marchantiophyta, Pallaviciniaceae).";
 RL Bryologist 108:204-211(2005).
 DR EMBL; AY734732; AAX46221.1; -; Genomic_DNA.
 RT Chloroplast.
 KW FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1030 MW; 6D4E2727272451B4 CRC64;

Query Match 35.7%; Score 15; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LRDDL 7
 DB 1 MRTL 6

RESULT 12
 Q4QWV3_9MARC PRELIMINARY; PRT; 9 AA.
 ID Q4QWV3_9MARC PRELIMINARY; PRT; 9 AA.
 AC Q4QWV3;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE AtPB (Fragment).
 GN Name=atPB;
 OS *Jensenia spinosa*.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
 OC Jungermanniopsida; Metzgeriales; Metzgeriaceae; Pallaviciniaceae;
 OC Pallaviciniaceae; *Jensenia*.
 OC NCBI_TaxId=280534;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Forrest L.L., Schutte S.W., Crandall-Stotler B.J., Stotler R.E.;
 RT "A Molecular Study of the Simple Thalloid Liverwort *Jensenia*
 (Marchantiophyta, Pallaviciniaceae).";

RL Bryologist 108:204-211(2005).
 DR EMBL; AY734726; AAX46211.1; -; Genomic_DNA.
 KW FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1030 MW; 6D4E2727272451B4 CRC64;

Query Match 35.7%; Score 15; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LRDDL 7
 DB 1 MRTL 6

RESULT 13
 P83539_LACSN PRELIMINARY; PRT; 9 AA.
 ID P83539_LACSN PRELIMINARY; PRT; 9 AA.
 AC P83539;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Unknown protein from 2D-page (Fragment).
 OS *Lactobacillus sanfranciscensis* (Lactobacillus sanfrancisco).
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OC NCBI_TaxId=1625;
 RN [1]
 RP PROTEIN SEQUENCE, AND INDUCTION.
 RA STRAIN=DSM 20451;
 RX DOI=10.1002/1615-9861(200206)2:6<765::AID-PROT765>3.0.CO;2-V;
 RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Georg A.;
 RT "High pressure effects step-wise altered protein expression in
Lactobacillus sanfranciscensis.";
 RL Proteomics 2:765-774(2002).
 CC -1- INDUCTION: By elevated hydrostatic pressure.
 CC -1- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
 protein is: 65 kDa.
 CC FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1099 MW; 707B2455B72AA734 CRC64;

Query Match 35.7%; Score 15; DB 2; Length 9;
 Best Local Similarity 80.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LRDDL 6
 DB 1 MRTL 5

RESULT 14
 Q51594_9ZZZZ PRELIMINARY; PRT; 8 AA.
 ID Q51594_9ZZZZ PRELIMINARY; PRT; 8 AA.
 AC Q51594;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE COPB Protein (Fragment).
 OS Plasmid ColV2-K94.
 OC Plasmid ColV2-K94.
 OC other sequences; plasmids.
 OC NCBI_TaxId=2458;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=86223772; PubMed=2423502;
 RA Weber P.C., Palchaudhuri S.;
 RT "Incompatibility repressor in a RepA-like replicon of the IncFI
 plasmid ColV2-K94.";
 RT J. Bacteriol. 166:1106-1112(1986).
 DR EMBL; M13472; AAA3194.1; -; Genomic_DNA.
 KW Plasmid.

FT NON TER 1 1
SQ SEQUENCE 8 AA; 998 MW; 0F37205AA73416D7 CRC64;

Query Match 33.3%; Score 14; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 RDDLE 8
| | | | |
Db 3 RDDLE 8

RESULT 15

08KPY4_9CHRO
ID 08KPY4_9CHRO PRELIMINARY; PRT; 8 AA.
AC 08KPY4;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DB Phycocyanin alpha subunit (Fragment).
GN Name=pca;
OS Microcystis sp. T96-1.
OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
OX NCBI_TaxID=198099;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22338268; PubMed=12450830;
RX DOI=10.1128/AEM.68.12.6070-6076.2002;
RA Baker J.A., Entsch B., Neilan B.A., McKay D.B.;
RT "Monitoring changing toxigenicity of a cyanobacterial bloom by
RT molecular methods";
RL Appl. Environ. Microbiol. 68:6070-6076(2002).
DR EMBL: AY117046; MAM54719.1; -; Genomic_DNA.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 890 MW; F4DB01A73771A336 CRC64;

Query Match 33.3%; Score 14; DB 2; Length 8;
Best Local Similarity 37.5%; Pred. No. 2.2e+06;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LRDDLLEA 9
: : | | | | |
Db 1 MKTPLEA 8

Search completed: April 6, 2006, 16:25:10
Job time : 120 secs

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US-09-489-760-5

Query Match 100.0%; Score 42; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLKDDLEA 9
DB 1 VLKDDLEA 9

RESULT 3
US-09-269-250E-20
; Sequence 20, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-20

Query Match 88.1%; Score 37; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLKDDLEA 9
DB 1 VLKDDLEA 9

RESULT 4
US-09-489-760-2
; Sequence 2, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leiden
; APPLICANT: Goulimy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Histocompatibility antigen
US-09-489-760-2

Query Match 88.1%; Score 37; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLKDDLEA 9
DB 1 VLKDDLEA 9

RESULT 5

US-09-269-250E-29

; Sequence 29, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
US-09-269-250E-29

Query Match 85.7%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLKDDLEA 9
DB 1 VLKDDLEA 9

RESULT 6
US-09-489-760-1
; Sequence 1, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leiden
; APPLICANT: Goulimy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Histocompatibility antigen
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (3)
; OTHER INFORMATION: AMINO ACID X REPRESENTS A HISTIDINE OR AN ARGININE
; OTHER INFORMATION: RESIDUE
US-09-489-760-1

Query Match 85.7%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLKDDLEA 9
DB 1 VLKDDLEA 9

RESULT 7
US-09-217-609A-11
; Sequence 11, Application US/09217609A
; Patent No. 6071733
; GENERAL INFORMATION:
; APPLICANT: MURAMATSU, Masayoshi

```

; APPLICANT: KOIKE, Ayumi
; APPLICANT: OGURA, Kyozo
; APPLICANT: KOYAMA, Tanetoshi
; APPLICANT: SHIMIZU, Naoto
; APPLICANT: CHO, Yewlin
; TITLE OF INVENTION: Prenyl Diphosphate Synthetase Genes
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, NW - Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: US
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
; SOFTWARE: Wordperfect 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,609A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/873,235
; FILING DATE: 11-Jun-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: TOFFENETTI, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 10235/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-1776
; TELEFAX: 202-429-0796
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-217-609A-11

Query Match          64.3%; Score 27; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.6e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 LRDDLE 8
       :|||:|:
Db      3 IRDDILD 9

RESULT 8
US-08-873-235B-11
; Sequence 11, Application US/08873235B
; Patent No. 6174715
; GENERAL INFORMATION:
; APPLICANT: MURAMATSU, Masayoshi
; APPLICANT: KOIKE, Ayumi
; APPLICANT: OGURA, Kyozo
; APPLICANT: KOYAMA, Tanetoshi
; APPLICANT: SHIMIZU, Naoto
; APPLICANT: CHO, Yewlin
; TITLE OF INVENTION: Prenyl Diphosphate Synthetase Genes
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, NW - Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: US
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
; SOFTWARE: Wordperfect 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,235B
; FILING DATE: 11-Jun-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 154441/1996
; FILING DATE: 14-Jun-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: TOFFENETTI, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 10235/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-0796
; TELEFAX: 202-429-1776
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-873-235B-11

Query Match          64.3%; Score 27; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.6e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 LRDDLE 8
       :|||:|:
Db      3 IRDDILD 9

RESULT 9
US-09-269-250E-38
; Sequence 38, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patencin version 3.1
; SEQ ID NO 38
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN
; US-09-269-250E-38

Query Match          54.8%; Score 23; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 DLEEA 9
       |||||
Db      4 DLEEA 8

RESULT 10
US-08-556-419-14
; Sequence 14, Application US/08556419C
; Patent No. 6093549
; GENERAL INFORMATION:
; APPLICANT: Ross, Christopher
; APPLICANT: Li, Xiao-Jiang
; APPLICANT: Li, Shi-Hua
; APPLICANT: Sharp, Alan
; APPLICANT: Ianahan, Anthony
; APPLICANT: Worley, Paul
; APPLICANT: Snyder, Solomon
; TITLE OF INVENTION: Huntingtin-associated protein
```

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; FILE REFERENCE: 01107.52271
; CURRENT APPLICATION NUMBER: US/08/556,419C
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-08-556-419-14

Query Match
Best Local Similarity 52.4%; Score 22; DB 2; Length 7;
Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8
Db 1 DDLE 5

RESULT 11
US-09-489-760-4
; Sequence 4, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leiden
; APPLICANT: Goulimy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Histocompatibility antigen
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (2)..(7)
; OTHER INFORMATION: AMINO ACIDS X REPRESENT LEUCINE OR ISOLEUCINE
; OTHER INFORMATION: RESIDUES
US-09-489-760-4

Query Match
Best Local Similarity 52.4%; Score 22; DB 2; Length 9;
Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 VLRDLEA 9
Db 1 VXHDXKXA 9

RESULT 12
US-08-459-568-20
; Sequence 20, Application US/08459568
; Patent No. 5811304
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,568
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-459-568-20

Query Match
Best Local Similarity 50.0%; Score 21; DB 1; Length 6;
Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8
Db 1 DDLE 5

RESULT 13
US-08-399-411-20
; Sequence 20, Application US/08399411
; Patent No. 5831008
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,411
; FILING DATE: 06-MAR-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-399-411-20
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Query Match 50.0%; Score 21; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0;

QY 4 DDLE 8
: ||||
DB 1 EDLE 5

RESULT 14

US-08-516-859A-20
; Sequence 20, Application US/08516859A
; Patent No. 6069231
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/516,859A
; FILING DATE: 18-AUG-1995
; CLASSIFICATION: 514
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1776
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-516-859A-20

Query Match 50.0%; Score 21; DB 2; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0;

QY 4 DDLE 8
: ||||
DB 1 EDLE 5

RESULT 15

US-09-586-472-20
; Sequence 20, Application US/09586472
; Patent No. 6323335
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/586,472
FILING DATE: 01-Jun-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/528,706
FILING DATE: 17-MAR-2000
APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 4130
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-586-472-20

Query Match 50.0%; Score 21; DB 2; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0;

QY 4 DDLE 8
: ||||
DB 1 EDLE 5

Search completed: April 6, 2006, 16:27:37
JOB time : 27.6667 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:44:31 ; Search time 90.333 Seconds
(without alignments)
41.629 Million cell updates/sec

Title: US-10-791-217A-5
Perfect score: 42
Sequence: 1 VLRDDLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 180914

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBSCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBSCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBSCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBSCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	9	4	US-10-623-176-10 Sequence 10, Appl
2	42	100.0	9	4	US-10-791-217-5 Sequence 5, Appl
3	42	100.0	9	6	US-11-007-740-18 Sequence 18, Appl
4	38	90.5	9	4	US-10-623-176-42 Sequence 42, Appl
5	38	90.5	9	4	US-10-623-176-46 Sequence 46, Appl
6	37	88.1	9	4	US-10-623-176-2 Sequence 2, Appl
7	37	88.1	9	4	US-10-791-217-2 Sequence 2, Appl
8	37	88.1	9	5	US-10-861-335-1 Sequence 20, Appl
9	37	88.1	9	6	US-11-007-740-20 Sequence 1, Appl
10	36	85.7	9	4	US-10-623-176-1 Sequence 1, Appl
11	36	85.7	9	4	US-10-791-217-1 Sequence 29, Appl
12	36	85.7	9	6	US-11-007-740-29 Sequence 48, Appl
13	34	81.0	9	4	US-10-623-176-48 Sequence 23, Appl
14	33	78.6	9	4	US-10-623-176-23 Sequence 41, Appl
15	33	78.6	9	4	US-10-623-176-41 Sequence 45, Appl
16	33	78.6	9	4	US-10-623-176-45 Sequence 47, Appl
17	29	69.0	9	4	US-10-623-176-5 Sequence 4, Appl
18	29	69.0	9	4	US-10-623-176-47 Sequence 39, Appl
19	28	66.7	9	4	US-10-623-176-40 Sequence 349, App
20	25	59.5	9	3	US-09-834-765-349 Sequence 16, Appl
21	25	59.5	7	4	US-10-623-176-39 Sequence 4, Appl
22	24	57.1	9	4	US-10-271-708-16 Sequence 16, Appl
23	24	57.1	9	4	US-10-623-176-4 Sequence 26, Appl
24	24	57.1	9	5	US-10-503-135-26 Sequence 64, Appl
25	24	57.1	9	5	US-10-503-135-64 Sequence 15, Appl
26	23	54.8	8	4	US-10-623-176-15 Sequence 38, Appl
27	23	54.8	8	6	US-11-007-740-38 Sequence 38, Appl

ALIGNMENTS

28	23	54.8	9	3	US-09-834-765-132 Sequence 132, App
29	23	54.8	9	4	US-10-623-176-3 Sequence 3, Appl
30	22	52.4	9	4	US-10-623-176-14 Sequence 14, Appl
31	22	52.4	9	4	US-10-791-217-4 Sequence 4, Appl
32	22	52.4	9	6	US-11-007-740-40 Sequence 40, Appl
33	21	50.0	7	3	US-09-990-186-208 Sequence 208, App
34	21	50.0	7	3	US-09-990-186-211 Sequence 211, App
35	21	50.0	7	3	US-09-990-186-216 Sequence 216, App
36	21	50.0	7	3	US-09-989-994-208 Sequence 208, App
37	21	50.0	7	3	US-09-989-994-211 Sequence 211, App
38	21	50.0	7	3	US-09-989-994-216 Sequence 216, App
39	21	50.0	7	4	US-10-122-675-6 Sequence 6, Appl
40	21	50.0	7	5	US-10-487-268-9 Sequence 9, Appl
41	21	50.0	8	4	US-10-700-330-169 Sequence 169, App
42	21	50.0	9	3	US-09-935-430-219 Sequence 219, App
43	21	50.0	9	3	US-09-935-430-565 Sequence 565, App
44	21	50.0	9	3	US-09-833-203-54 Sequence 54, Appl
45	21	50.0	9	4	US-10-119-536A-109 Sequence 109, Appl

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RESULT 1
US-10-623-176-10
; Sequence 10, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elia A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-10
Query Match 100.0%; Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. NO. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 VLRDDLEA 9
Db 1 VLRDDLEA 9
RESULT 2
US-10-791-217-5
; Sequence 5, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elia A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Engelhard, Victor H
```

;; TITLE OF INVENTION: The HA-1 Antigen
;; FILE REFERENCE: 2183-4285US
;; CURRENT APPLICATION NUMBER: US/10/791,217
;; CURRENT FILING DATE: 2004-03-02
;; PRIOR APPLICATION NUMBER: US/09/489,760
;; PRIOR FILING DATE: 2000-01-21
;; PRIOR APPLICATION NUMBER: PCT/NL98/00424
;; PRIOR FILING DATE: 1998-07-23
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 5
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: obtained from KIAA0223 partial complementary DNA
US-10-791-217-5

Query Match 100.0%; Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLRDDLEA 9
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Db 1 VLRDDLEA 9

RESULT 3
US-11-007-740-18
; Sequence 18, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 2799/58994-A
; CURRENT APPLICATION NUMBER: US/11/007,740
; CURRENT FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: 09/269,250
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-18

Query Match 100.0%; Score 42; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLRDDLEA 9
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Db 1 VLRDDLEA 9

RESULT 4
US-10-623-176-42
; Sequence 42, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0

;; PRIOR FILING DATE: 1997-07-23
;; PRIOR APPLICATION NUMBER: PCT/NL98/00424
;; PRIOR FILING DATE: 1998-07-23
;; PRIOR APPLICATION NUMBER: JP 2000-504165
;; PRIOR FILING DATE: 2000-01-24
;; NUMBER OF SEQ ID NOS: 77
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 42
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;; NAME/KEY: SITE
;; LOCATION: (1)..(9)
US-10-623-176-42

Query Match 90.5%; Score 38; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLRDDLE 8
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Db 2 VLRDDLE 9

RESULT 5
US-10-623-176-46
; Sequence 46, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;; NAME/KEY: SITE
;; LOCATION: (1)..(9)
US-10-623-176-46

Query Match 90.5%; Score 38; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRRDDLEA 9
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Db 1 LRRDDLEA 8

RESULT 6
US-10-623-176-2
; Sequence 2, Application US/10623176
; Publication No. US20040092446A1

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/ GENERAL INFORMATION:
/ APPLICANT: Goulmy, Els A.J.M.
/ APPLICANT: Hunt, Donald F.
/ APPLICANT: Engelhard, Victor H.
/ TITLE OF INVENTION: HA-1 epitopes and uses thereof
/ FILE REFERENCE: 2183-6047US
/ CURRENT APPLICATION NUMBER: US/10/623,176
/ CURRENT FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: 09/489,760
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: EP 97202303.0
/ PRIOR FILING DATE: 1997-07-23
/ PRIOR APPLICATION NUMBER: PCT/NL98/00424
/ PRIOR FILING DATE: 1998-07-23
/ PRIOR APPLICATION NUMBER: JP 2000-504165
/ PRIOR FILING DATE: 2000-01-24
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
/ NAME/KEY: SITE
/ LOCATION: (1)..(9)
US-10-623-176-2
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Query Match      88.1%; Score 37; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 VLHDDLEA 9
      |||||
      1 VLHDDLEA 9

RESULT 7
US-10-791-217-2
/ Sequence 2, Application US/10791217
/ Publication No. US20040191268A1
/ GENERAL INFORMATION:
/ APPLICANT: Goulmy, Elsa A.J.M
/ APPLICANT: Hunt, Donald F
/ APPLICANT: Engelhard, Victor H
/ TITLE OF INVENTION: The HA-1 Antigen
/ FILE REFERENCE: 2183-4285US
/ CURRENT APPLICATION NUMBER: US/10/791,217
/ CURRENT FILING DATE: 2004-03-02
/ PRIOR APPLICATION NUMBER: US/09/489,760
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: PCT/NL98/00424
/ PRIOR FILING DATE: 1998-07-23
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: obtained from histocompatibility antigen
US-10-791-217-2
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```
Query Match      88.1%; Score 37; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 8
US-10-861-335-1
/ Sequence 1, Application US/10861335
/ Publication No. US20050031612A1
/ GENERAL INFORMATION:
/ APPLICANT: Goulmy, Elsa A.J.M.
/ TITLE OF INVENTION: Minor histocompatibility antigen HA-1: target antigen for immu
/ TITLE OF INVENTION: of tumors
/ FILE REFERENCE: 2183-6479US
/ CURRENT APPLICATION NUMBER: US/10/861,335
/ CURRENT FILING DATE: 2004-06-04
/ PRIOR APPLICATION NUMBER: PCT/NL02/00791
/ PRIOR FILING DATE: 2002-12-05
/ PRIOR APPLICATION NUMBER: EP 01204704.9
/ PRIOR FILING DATE: 2001-12-05
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: HA-1 peptide
US-10-861-335-1
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Query Match      88.1%; Score 37; DB 5; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 VLHDDLEA 9
      |||||
      1 VLHDDLEA 9

RESULT 9
US-11-007-740-20
/ Sequence 20, Application US/11007740
/ Publication No. US2005023350A1
/ GENERAL INFORMATION:
/ APPLICANT: Goulmy, Elsa
/ TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
/ FILE REFERENCE: 2799/58994-A
/ CURRENT APPLICATION NUMBER: US/11/007,740
/ CURRENT FILING DATE: 2004-12-08
/ PRIOR APPLICATION NUMBER: 09/269,250
/ PRIOR FILING DATE: 1999-05-21
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 20
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-20
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Query Match      88.1%; Score 37; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 VLHDDLEA 9
      |||||
      1 VLHDDLEA 9

RESULT 10
US-10-623-176-1
/ Sequence 1, Application US/10623176
/ Publication No. US20040092446A1
/ GENERAL INFORMATION:
/ APPLICANT: Goulmy, Els A.J.M.
/ APPLICANT: Hunt, Donald F.
/ APPLICANT: Engelhard, Victor H.
```

TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
CURRENT FILING DATE: 2003-07-18
PRIORITY APPLICATION NUMBER: 09/489,760
PRIORITY FILING DATE: 2000-01-21
PRIORITY APPLICATION NUMBER: EP 97202303.0
PRIORITY FILING DATE: 1997-07-23
PRIORITY APPLICATION NUMBER: PCT/NL98/00424
PRIORITY FILING DATE: 1998-07-23
PRIORITY APPLICATION NUMBER: JP 2000-504165
PRIORITY FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
NAME/KEY: SITE
LOCATION: (1)..(9)
US-10-623-176-1

Query Match 85.7%; Score 36; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
DB 1 VLXDDLLEA 9

RESULT 11
US-10-791-217-1
Sequence 1, Application US/10791217
Publication No. US20040191268A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Elsa A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: The HA-1 Antigen
FILE REFERENCE: 2183-4285US
CURRENT APPLICATION NUMBER: US/10/791,217
CURRENT FILING DATE: 2004-03-02
PRIORITY APPLICATION NUMBER: US/09/489,760
PRIORITY FILING DATE: 2000-01-21
PRIORITY APPLICATION NUMBER: PCT/NL98/00424
PRIORITY FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: obtained from histocompatibility antigen
NAME/KEY: MISC FEATURE
LOCATION: (3)..(3)
OTHER INFORMATION: Xaa is HISTIDINE OR ARGinine RESIDUE
US-10-791-217-1

Query Match 85.7%; Score 36; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
DB 1 VLXDDLLEA 9

RESULT 12
US-11-007-740-29
Sequence 29, Application US/11007740
Publication No. US2005023350A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Elsa
TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
FILE REFERENCE: 2799/58994-A
CURRENT APPLICATION NUMBER: US/11/007,740
CURRENT FILING DATE: 2004-12-08
PRIORITY APPLICATION NUMBER: 09/269,250
PRIORITY FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 9
TYPE: PRT
ORGANISM: Human
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (3)..(3)
OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
US-11-007-740-29

Query Match 85.7%; Score 36; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
DB 1 VLXDDLLEA 9

RESULT 13
US-10-623-176-48
Sequence 48, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Els A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
CURRENT FILING DATE: 2003-07-18
PRIORITY APPLICATION NUMBER: 09/489,760
PRIORITY FILING DATE: 2000-01-21
PRIORITY APPLICATION NUMBER: EP 97202303.0
PRIORITY FILING DATE: 1997-07-23
PRIORITY APPLICATION NUMBER: PCT/NL98/00424
PRIORITY FILING DATE: 1998-07-23
PRIORITY APPLICATION NUMBER: JP 2000-504165
PRIORITY FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 48
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
NAME/KEY: SITE
LOCATION: (1)..(9)
US-10-623-176-48

Query Match 81.0%; Score 34; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RDDDLLEA 9
DB 1 VLXDDLLEA 9

Db 1 RDDLLA 7

RESULT 14
US-10-623-176-23
; Sequence 23, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-23

Query Match 78.6%; Score 33; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLRDDLL 7
| | | | |
Db 3 VLRDDLL 9

RESULT 15
US-10-623-176-41
; Sequence 41, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide

; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-41

Query Match 78.6%; Score 33; DB 4; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLRDDLL 8
| | | | |
Db 2 VLHDDLL 9

Search completed: April 6, 2006, 16:50:29
Job time : 90.3333 secs

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OM protein - protein search, using SW model

Run on: April 6, 2006, 16:46:11 / Search time 12.333 Seconds
(without alignments)
22.762 Million cell updates/sec

Title: US-10-791-217A-5

Perfect score: 42
Sequence: 1 VLRDDLLRA 9

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 38721

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

Published Applications NA New:
1: /SIDSS/ptcodata/2/pubpaa/US08 NEW PUB pep: *
2: /SIDSS/ptcodata/2/pubpaa/US06 NEW PUB pep: *
3: /SIDSS/ptcodata/2/pubpaa/US07 NEW PUB pep: *
4: /SIDSS/ptcodata/2/pubpaa/PCT_NEW PUB pep: *
5: /SIDSS/ptcodata/2/pubpaa/US09 NEW PUB pep: *
6: /SIDSS/ptcodata/2/pubpaa/US10 NEW PUB pep: *
7: /SIDSS/ptcodata/2/pubpaa/US11 NEW PUB pep: *
8: /SIDSS/ptcodata/2/pubpaa/US60_NEW PUB pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	42	100.0	9	US-11-010-748A-12
2	37	88.1	9	US-11-010-748A-11
3	21	50.0	4	US-11-019-027-17
4	21	50.0	7	US-11-096-706-52
5	21	50.0	7	US-11-225-686-208
6	21	50.0	7	US-11-225-686-211
7	21	50.0	7	US-11-225-686-216
8	21	50.0	7	US-11-202-009-208
9	21	50.0	7	US-11-202-009-211
10	21	50.0	7	US-11-202-009-216
11	21	50.0	9	US-10-989-767A-219
12	21	50.0	6	US-10-989-767A-216
13	20	47.6	5	US-11-129-143-168
14	20	47.6	5	US-11-129-143-169
15	20	47.6	5	US-11-129-143-170
16	20	47.6	5	US-11-129-143-171
17	20	47.6	5	US-11-129-143-172
18	20	47.6	5	US-11-129-143-173
19	20	47.6	7	US-10-982-440-126
20	20	47.6	7	US-11-096-706-88
21	20	47.6	7	US-11-096-706-164
22	20	47.6	8	US-11-021-305-62
23	20	47.6	8	US-11-021-305-65
24	20	47.6	8	US-11-021-305-66
25	20	47.6	9	US-10-927-435-63

26	20	47.6	9	US-10-927-634-63	Sequence 63, Appl
27	19	45.2	7	US-11-225-686-2954	Sequence 2954, Ap
28	19	45.2	7	US-11-225-686-3877	Sequence 3877, Ap
29	19	45.2	7	US-11-225-686-3914	Sequence 3914, Ap
30	19	45.2	7	US-11-225-686-3915	Sequence 3915, Ap
31	19	45.2	7	US-11-225-686-3916	Sequence 3916, Ap
32	19	45.2	7	US-11-225-686-3917	Sequence 3917, Ap
33	19	45.2	7	US-11-225-686-3918	Sequence 3918, Ap
34	19	45.2	7	US-11-202-009-2954	Sequence 2954, Ap
35	19	45.2	7	US-11-202-009-3877	Sequence 3877, Ap
36	19	45.2	7	US-11-202-009-3914	Sequence 3914, Ap
37	19	45.2	7	US-11-202-009-3915	Sequence 3915, Ap
38	19	45.2	7	US-11-202-009-3916	Sequence 3916, Ap
39	19	45.2	7	US-11-202-009-3917	Sequence 3917, Ap
40	19	45.2	7	US-11-202-009-3918	Sequence 3918, Ap
41	19	45.2	8	US-11-045-024-575	Sequence 575, App
42	19	45.2	8	US-11-045-024-3138	Sequence 3138, Ap
43	19	45.2	8	US-11-045-024-3698	Sequence 3698, Ap
44	19	45.2	8	US-11-045-024-5495	Sequence 5495, Ap
45	19	45.2	8	US-11-045-024-5716	Sequence 5716, Ap

ALIGNMENTS

RESULT 1
US-11-010-748A-12
Sequence 12, Application US/11010748A
Publication No. US20050244421A1
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMAYER, Wolfgang
APPLICANT: MOLL, Heidrun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
FILE REFERENCE: MER-136
CURRENT APPLICATION NUMBER: US/11/010,748A
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/EP03/06251
PRIOR FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: EP02013423.5
PRIOR FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 926
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(9)
OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T
US-11-010-748A-12
Query Match 100.0%; Score 42; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLRDDLLRA 9
DB 1 VLRDDLLRA 9
RESULT 2
US-11-010-748A-11
Sequence 11, Application US/11010748A
Publication No. US20050244421A1
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMAYER, Wolfgang
APPLICANT: MOLL, Heidrun
APPLICANT: SCHAM, Burkhard

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
;; FILE REFERENCE: MER-136
;; CURRENT APPLICATION NUMBER: US/11/010,748A
;; CURRENT FILING DATE: 2004-12-13
;; PRIOR APPLICATION NUMBER: PCT/EP03/06251
;; PRIOR FILING DATE: 2003-06-13
;; PRIOR APPLICATION NUMBER: EP02013423.5
;; PRIOR FILING DATE: 2002-06-13
;; NUMBER OF SEQ ID NOS: 926
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 11
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (1)..(9)
;; OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
US-11-010-748A-11

Query Match 88.1%; Score 37; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VRDILLEA 9
DB 1 VADILLEA 9

RESULT 3
US-11-019-027-17
;; Sequence 17, Application US/11019027
;; Publication No. US20050282181A1
;; GENERAL INFORMATION:
;; APPLICANT: VAN, Wei
;; APPLICANT: SHEN, Mengyan
;; APPLICANT: ZHOU, Hongxing
;; APPLICANT: ZHOU, Chen
;; APPLICANT: COSMAN, David J.
;; APPLICANT: CARTER, Paul
;; APPLICANT: MARTIN, Francis H.
;; TITLE OF INVENTION: METHODS OF IDENTIFYING FUNCTIONAL ANTIBODIES
;; FILE REFERENCE: A-890A
;; CURRENT APPLICATION NUMBER: US/11/019,027
;; CURRENT FILING DATE: 2004-12-21
;; PRIOR APPLICATION NUMBER: 60/605,902
;; PRIOR FILING DATE: 2004-08-31
;; PRIOR APPLICATION NUMBER: 60/531,714
;; PRIOR FILING DATE: 2003-12-22
;; NUMBER OF SEQ ID NOS: 73
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 17
;; LENGTH: 4
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: ER localization signal
US-11-019-027-17

Query Match 50.0%; Score 21; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RDDL 6
DB 1 RDDL 4

RESULT 4
US-11-096-706-52
;; Sequence 52, Application US/11096706
;; Publication No. US20050245476A1

;; GENERAL INFORMATION:
;; APPLICANT: Sangamo Biosciences, Inc.
;; APPLICANT: Collingwood, Trevor
;; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
;; FILE REFERENCE: 019496-008200S
;; CURRENT APPLICATION NUMBER: US/11/096,706
;; CURRENT FILING DATE: 2005-04-01
;; PRIOR APPLICATION NUMBER: US 60/560,535
;; PRIOR FILING DATE: 2004-04-08
;; PRIOR APPLICATION NUMBER: US 60/576,757
;; PRIOR FILING DATE: 2004-06-02
;; NUMBER OF SEQ ID NOS: 227
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 52
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein recognition
US-11-096-706-52

Query Match 50.0%; Score 21; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RDDL 6
DB 2 RDDL 5

RESULT 5
US-11-225-686-208
;; Sequence 208, Application US/11225686
;; Publication No. US20060019349A1
;; GENERAL INFORMATION:
;; APPLICANT: LIU, Qiang
;; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;; FILE REFERENCE: 8325-0011.20 / S11-US2
;; CURRENT APPLICATION NUMBER: US/11/225,686
;; CURRENT FILING DATE: 2005-09-12
;; PRIOR APPLICATION NUMBER: US/09/989,994
;; PRIOR FILING DATE: 2001-11-20
;; NUMBER OF SEQ ID NOS: 4085
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 208
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-11-225-686-208

Query Match 50.0%; Score 21; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RDDL 8
DB 1 RDDL 6

RESULT 6
US-11-225-686-211
;; Sequence 211, Application US/11225686
;; Publication No. US20060019349A1
;; GENERAL INFORMATION:
;; APPLICANT: LIU, Qiang
;; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;; FILE REFERENCE: 8325-0011.20 / S11-US2
;; CURRENT APPLICATION NUMBER: US/11/225,686


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; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example zfp
US-11-225-686-211

Query Match
Best Local Similarity 50.0%; Score 21; DB 7; Length 7;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RDDLE 8
   | |||:
Db 1 RSDLLQ 6

RESULT 7
US-11-225-686-216
; Sequence 216, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 216
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example zfp
US-11-225-686-216

Query Match
Best Local Similarity 50.0%; Score 21; DB 7; Length 7;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RDDLE 8
   | |||:
Db 1 RSDLLQ 6

RESULT 8
US-11-202-009-208
; Sequence 208, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 208
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example zfp
US-11-202-009-208

Query Match
Best Local Similarity 50.0%; Score 21; DB 7; Length 7;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RDDLE 8
   | |||:
Db 1 RSDLLQ 6

RESULT 9
US-11-202-009-211
; Sequence 211, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example zfp
US-11-202-009-211

Query Match
Best Local Similarity 50.0%; Score 21; DB 7; Length 7;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RDDLE 8
   | |||:
Db 1 RSDLLQ 6

RESULT 10
US-11-202-009-216
; Sequence 216, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 216
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example zfp
US-11-202-009-216

Query Match
Best Local Similarity 50.0%; Score 21; DB 7; Length 7;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RDDLE 8
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Db 1 RSDLD 6

RESULT 11
US-10-989-767A-219

; Sequence 219, Application US/10989767A

; Publication No. US20060018917A1

; GENERAL INFORMATION:

; APPLICANT: FARIS, MARY

; APPLICANT: HUBERT, RENE

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: AFAR, DANIEL

; APPLICANT: LEVIN, ELANA

; APPLICANT: CHALILTA-EID, PIA

; APPLICANT: JAKOBOVITZ, AYA

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7

; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND

; FILE REFERENCE: 511582005004

; CURRENT APPLICATION NUMBER: US/10/989,767A

; CURRENT FILING DATE: 2004-11-15

; PRIOR APPLICATION NUMBER: 10/277,292

; PRIOR FILING DATE: 2002-10-21

; PRIOR APPLICATION NUMBER: 09/935,430

; PRIOR FILING DATE: 2001-08-22

; PRIOR APPLICATION NUMBER: 60/227,098

; PRIOR FILING DATE: 2000-08-22

; PRIOR APPLICATION NUMBER: 60/282,739

; PRIOR FILING DATE: 2001-04-10

; NUMBER OF SEQ ID NOS: 700

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 219

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Chemically synthesized peptide motif

US-10-989-767A-219

Query Match 50.0%; Score 21; DB 6; Length 9;
Best Local Similarity 37.5%; Pred. No. 1.4e+05;

Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 VRDLDL 8
Db 1 LKMSDLVE 8

RESULT 12
US-10-989-767A-565
; Sequence 565, Application US/10989767A
; Publication No. US20060018917A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALILTA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 511582005004
; CURRENT APPLICATION NUMBER: US/10/989,767A
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: 10/277,292
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22

; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 565
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide motif

US-10-989-767A-565

Query Match 50.0%; Score 21; DB 6; Length 9;
Best Local Similarity 37.5%; Pred. No. 1.4e+05;

Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 VRDLDL 8
Db 1 LKMSDLVE 8

RESULT 13
US-11-129-143-168
; Sequence 168, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBLIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Bradyrhizobium japonicum
; OTHER INFORMATION: Chemically synthesized peptide motif

US-11-129-143-168

Query Match 47.6%; Score 20; DB 7; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLDL 8
Db 1 DDLDL 5

RESULT 14
US-11-129-143-169
; Sequence 169, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBLIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 169
; LENGTH: 5
; TYPE: PRT

US-11-129-143-169

Query Match 47.6%; Score 20; DB 7; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLDL 8
Db 1 DDLDL 5

RESULT 14
US-11-129-143-169
; Sequence 169, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBLIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 169
; LENGTH: 5
; TYPE: PRT

US-11-129-143-169

Query Match 47.6%; Score 20; DB 7; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLDL 8
Db 1 DDLDL 5

RESULT 14
US-11-129-143-169
; Sequence 169, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBLIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 169
; LENGTH: 5
; TYPE: PRT

US-11-129-143-169

Query Match 47.6%; Score 20; DB 7; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLDL 8
Db 1 DDLDL 5

RESULT 14
US-11-129-143-169
; Sequence 169, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBLIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 169
; LENGTH: 5
; TYPE: PRT

US-11-129-143-169

ORGANISM: Rhizobium sp. strain NGR234
US-11-129-143-169

Query Match 47.6%; Score 20; DB 7; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8
|||:
Db 1 DDLD 5

RESULT 15

US-11-129-143-170
; Sequence 170, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-11-129-143-170

Query Match 47.6%; Score 20; DB 7; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8
|||:
Db 1 DDLD 5

Search completed: April 6, 2006, 16:51:12
Job time : 12.3333 secs

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